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(without alignments)
10481.029 Million cell updates/sec
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3742
1 gaattccattgtgttgggta......tgggatcctaaaaaaaaa 2043
                                                                                             ; Search time 37.5 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                               using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Sequence:
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Command line parameters:
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-Q=/cgnz 1/USF70_spool_p/US09645078/runat 06052004_104600_21755/app_query.fasta_1.2183
-DB=P.R 78 -QFWT=fastan_SUFFRIX=rpr -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-OCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptc -NORN=ext -HEAFSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRE-US09645078 @CGN 1 1.52 @runat .D6052004 104600 21755 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQÜERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:* Jatabase

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES		-	Description	N-acetylglucosamin	N-acetylglucosamin	N-acetylglucosamin	chondroitin 6-sulf	probable enzyme, C	BHLF1 protein - hu	collagen alpha 1(I	collagen alpha 1(I	thrombospondin 2 p	collagen alpha 1(I	FB19 protein - hum	collagen alpha 2(I	collagen alpha 1(I	hypothetical prote
SUMMARIES			ID	JC7350	JC7351	JE0261	A57397	E95934	QQBE3	S21626	CGHU1S	TSHUP2	859856	JE0291	A43291	CGHU6C	F75420
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		Query	Length	484	486	484	458	307	660	1453	1464	1172	1464	940	1373	1487	319
	æ	Query	Match	16.8	16.4	15.7	13.4	4.5	4.0	4.0	3.9	3.8	3.8	3.7	3.7	3.7	3.7
		,	Score	628.5	615.5	588.5	500.5	168	147	147	145	143.5	140.5	138.5	138.5	138.5	138
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ALIGNMENTS

RESULT 1

N-acetylglucosamine-6-O-gulfotransferase (EC 2.8.2.-) [validated] - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 31-Dec-2000
C;Accession: 407350
R;Uchimura, K.; Fasakhany, F.; Kadomatsu, K.; Matsukawa, T.; Yamakawa, T.; Kurosawa, N.;
B;Uchimura, B.Ophys. Res. Commun. 274, 291-296, 2000
A;Title: Diversity of N-acetylglucosamine-6-0-sulfotransferases: Molecular cloning of a A;Reference number: 407350
A;Accession: 407350
A;Accession: 407350
A;Accession: 407350
A;Accession: 407350
C;Comment: This ences: DDBJ;Ab040710
C;Comment: This ences: DDBJ;Ab040710
C;Comment: This encyme, having a type II transmembrane topology and N-linked glycosylatisulface linkage formation: This enzyme is involved in synthesis of L-selectin ligand in C;Keywords: glycolysis; sulfate transport; sulfotransferase; transmembrane protein

Alignment Scores:			
Pred. No.:	2.22e-39	Length:	484
Score:		Matches:	154
Percent Similarity:		Conservative:	71
Best Local Similarity:	33.05%	Mismatches:	177
Ouery Match:		Indels:	64
DB:		Gaps:	11

US-09-645-078-1 (1-2043) x JC7350 (1-484)

ò	19 TACGGAAGACGACAGAAGGGTAGAGAAAAAGCGCATGGCCCGGCTAGCAGTG 72
Db	AsnCysProG
λŏ	73 AGCCTCTCAAAAGCAGCAGGGAAGCCCAAGGCCTTCCACTTCAGCACAATGCT 132
DP	nglyAlaglı
à	133 ACTION DE DE DE DE DE DE DE CONTRONDE DE CONTRONDE DE LE 192

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erProGlySer 84 CAGCCGAGCG 252 :	. ც ⊢		PGGGCCGTCTT 432		. A GCCGGGCCCT 522 A A SSNLV8Valii 199 A A	570	630	69 25	750			ACTAT 859 Q ::: D spPhePheLe 339				ACGCTTTCCA 1089 Q. Q. L.	
75	253 CATGCACGTGCTGGTCTTCCTGGCGCTCTGGCTCTTTTTTGTGGGGCAGCTTTT	313 TGGGCAGCACCCAGATGTTTTCTACCTGATGGAGCCCGCCTGGCACGTGTGAATGACCTT	373 CAAGCAGACCCGCCTGGATGCTGCACATGGCTGTGCGGGATCTGATACGGCCCGTCTT 	433 CTTGTGCGACATGAGCGTCTTTGATGCCTACATGGAACCTGGTCCCCGGAGACAG 	488	523 GTGTTCTGCACCTGCCTGTGACATCCACACAAGATGAAATCATCCC :	571 CCGGGCTCACTGCAGGCTCCTGTGCAGTCAACAGCCCTTTGAGGTGGAGGGCGTGGT	631 CCGCTCCTACACCACGTGGTGCTCAAGGAGGTGGTTCTTCAACCTGCAGTCCTCTA	691 CCGGCTGGTGAAAGACCCCTCCTCAACCTGCATATGTGCACCTGGTCGGGACCCCGGGACCCCGGGACCCCGGGACCCCGGGACCCCGGGACCCCGGGACACGACG	751 GGCCGTGTTCCGGTTCCCGAGAACGCACAAAGGGAGATCTCATGATGACAGT	803	815GGGCAGCATGAGCAAAAACTCAAGAAGGAGGACCAACCCTACTAT 	860GTGATGCAGGTCATCTGCCAAAGCCAGCTGGAGATCTACAAGACCAGTC :::::	913 CTTGCCCAAGGCCCTGCAGGAACGCTACCTGCTTGTGCGCTATGAGGACCTGGCTCGAGC 359 yAlaProAlaTrpLeuArgArgArgTyrLeuArgLeuArgTyrGluAspLeuValTrpGl	973 CCCTGTGGCCCAGACTTCCCGAALGTATGAATTCGTGGGATTGGAATTCTTGCCCCATCT 	1033 TCAGACCTGGGTGCATAACATCACCGGAGGGAAGGGCATGGGTGACCACGTTTTCCA 	090 CACAAATGCCAGGGATGCCCTTAATGTCTCCCAGGCTTGGCGGTCTTTGCCCTATGA :::
op Oy O	<i>₹</i>	& g	Qy	oy Db	Qý	& g	& 43	S ea	Qy Db	67 07 07	QV Dp	Qy Db	. QQ	oy ab	ov e	Qy 10 Db	Oy 10

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O'CYSTALORSAMINE-6-O-sulfotransferase (EC 2.8.2.-) [validated] - human C'Species: Homo sapiens (man) ("Species: Homo sapiens ("Species: Homo sap
1150 AAAGGTTTCTCGACTTCAGAAAGCCTGTGGCGATGCCATGAATTTGCTGGGCTACCGCCA 1209
                                                                                                                                        459 gSerGlyAspGluArgAspArgLysThrValArgGluGlyGluThrProLeuGluThrLy 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 GCAGTG---AGCCTCTCAAAAGCAGCAAAGCCCAAGCCAAAGGTCTTCCACTTCAG 123
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                             ----CTGGATCTTCT
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53 GlyValTrpSerLeuGluAlaAlaAlaAlaGlyGluArgGluGlnGlyAlaGluAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATTGTGTTGGGTACGGAAGACGACAGAAGGGTAGAGGAAAAAGCGCATGGCCCCGGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 CACAATGCTACTGCCTAAAAAATGAAGCTCCTGCTGTTTCTGGTTTCCCAGATGGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AlaAlaGluGluGlyGlyAlaAsnGlnSerProArg------PheProSerAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 CTTGGCTCTATTCTTCCACATGTACAGCCACAACATCAGCTCCCTGTCTATGAAGGCACA
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                                                                                                     CGTCAGATCTGAACAAGAACAGAAACCTGTTG------
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Matches:
Conservative:
Mismatches:
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Gaps:
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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o d	481 GAGACAG	A:Wolecule type: mRNA A:Residues: 1-484 «UCH» A:Cross-references: DDBJ-AB014679 C.Commant: This protein catalyase the transfer of sulfate from 3'-phosphoadenc
oy Pa	514 CCGGGCCCTGTGTTCTGCACCTGCCTGTGACATCATCCCACAAGATGAA 562 ::: ::: 11 11 1	formation of the format
oy G	563 -ATCATCCCCCGGGCTCACTGCAGGCTCCTGTGCAGTCAACAGCCCTTTGAGGTGGTGA 621	Alignment Scores: 2.34e-36 Length: 484 Pred. No.: 588.50 Matches: 131 Percent Similarity: 54.40% Conservative: 67
8 1	GAAGGCCTGCCGCTCCTACAGCCACGTGGTGCTCAAGGAGGTGCGCTTCTTCAACCTGCA	35.99% Mismatches: 15.73% Indels: 2 Gaps:
a è	238 uAladiuCysArgLysTyrFroValValIleLysAspValArgLeuLeuAspLeuG 258	US-09-645-078-1 (1-2043) x JE0261 (1-484)
3 8	yvalLeuValProLeuLeuArgAspProGlyLeuAsnLeuLysValValGlnLeuPheAr	Oy 248 GAGCGCAIGCACGIGCTGCTICTTICTGGGGCTCTGGCTCTTTTTTGTGGGGCAG 307
<u>ک</u> ۾	742 GGACCCCGGGCCGTGTTCCGTGAGAACGCACAAAGGGAGATCTCATGATTGACAG 801	308 CTITITGGGCAGCACCCAGAIGTITICTACCTGATGGAGCCGGCCTGGCACGTGTGGTG 36
8		Db 137 LeupheAsnGlnAsnProGluValPhePheLeuTyrGluProValTrpHisValTrpGln 156 Ov 368 accmpcaacacacacacacacacacacacacacacacaca
q .		157 LysteuTyrProGlyAspAlaValSerLeuGlnGlyAlaAlaArgAspMetLeuSerAla
r d	318 sGlyValGlyAlaArgProdlyGlnSerArgAlaLeuProAlaAlaProArgAlaAs 338	dy 428 GTCTTCTTGTGCGACATGAGCGTCTTTGATGCCTACATGGAACCTGGTCCCCGGAGACAG 487
& 8		Deutytatgytybaspueusetvalfinedinibeutytseifilohiaditydelditydiydiydiydiydiydiydiydiydiydiydiydiydiy
ò	CATCCAGTCCTTCCTAAAGGCCTGCAGGAACGTTCTTCTTCTTCTTCTTTTTTTT	Db 197 AsnLeuThrThrLeuGlyllePheGlyAlaAlaThrAsnLysValValCysSerSerPro 216
qq	eAlaArgGlyAlaProAlaTrpLeuArgArgArgTyrLeuArgLeuArgTyrGluAspLe 37	occidentations of the control of the
දු දු	964 GGCTCGAGCCCTGTGGCCGACTTCCCGAATGTATGAATTGTGGGGATTGGAATTCTT 1023 1	593IGCAGTCAACAGCCCTITGAGGIGGTGGAGAAGGCCTGCCGGTCCTACAGCCACGTG 64
λŏ	1024 GCCCCATCTTCAGACCTGGGTGCATAACATCACCGAGGCAAGGGCATGGGTGACCA 1080	Db 236 LysCysProProGinArgheuAlaArgPheGludluGluCysArgLysTyrArgThrLeu 255 Ov 650 GIGCTCAAGGAGGTGCGCTTCTTCAACCTGCAGTCCCTCTTACCGCTGCTGAAAGACCCC 709
ପ୍	ualaalaLeuaspalaPhealaLeuasmetThrargGlyalaalaTyrGlyalaaspar 41	256 ValileLysGlyValArgValPheAspValAlaValLeuAlaProLeuLeuArgAspPro
දි දි	1081 CGCTTTTCCACAAATGCCAGGAATGCCTTTAATGTCTCCCAGGTTGGGGGTGGTCTTT 1140 418 GPropheHisleuseralaargaspalaargGalualaValHisAlaTrpArgGluargLe 438	710 ICCCTCAACCTGCAACGTGCACCTGGTCCGGGACCCCGGGGCGTGTTCCGATTCCCGA 76
ò	1141 GCCCTATGAAAAGTTTCTCGACTTCAGAAAGCCTGTGGCGATGCCATGAATTTGCTGGG 1200	276
qa		GANGGALANGGARAN CICALGALIGACAN INTERACTOR CAN INTER
දු දු	1201	815
RESULT		316 ArgAlaHisArgMetProPheLeuGluAlaAlaGI
N-acety C, Speci	2) - human	Db 336 GlyValGlyGroAnaryTyrHisAlaLeuGlyAlaMetGluValIleCysAssSer 355
C, Dare C, Acces R, Uchin	: O's TELLINGS # #sequence_revision O's Tellings # telkinduge of main 2002 saion: 180261 mura, K.; Muramatsu, H.; Kaname, T.; Ogawa, H.; Yamakawa, T.; Fan, Q.W.; Mitsuoka,	884 CAGCIGGAGAICIACAAGACCAICCAGICCITGCAAGGACACAGAACGCTACCIG 94
T. G. Bioc	And the state of t	356 MetAlaLy
A;Refel		Db 376 ValValArgTyrGluAspLeuValGlyGluProValLysThrLeuArgArgValTyrAsp 395

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probable enzyme, C-terminal domain similar to sulfotransferase protein [imported] - Sino C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Accession: B95934
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb psymB megaplasmid from the N2-fixing endo A;Reference number: A95842; MUID:21395508; PMID:11481431
A;Reference number: A95842; MUID:21395508; PMID:11481431
A;Residues: Drah.
A;Residues: Drah.
A;Residues: Drah.
A;Residues: L-307 - KURP.
A;Residues: Rain, P.; Coxie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T.
C: Hyman, R.W.; Jones, T.
C: Hyman, R.W.; Jones, T.
C: Lelaure, Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Weils, Yeh, K.
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Chondroitin 6-sulfotransferase (EC 2.8.2.17) precursor - chicken

chondroitin 6-sulfotransferase (EC 2.8.2.17) precursor - chicken

Chondroitin 6-sulfotransferase (EC 2.8.2.17) precursor - chicken

CjSpecies Gallus gallus (chicken)

CjDate: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 20-Jun-2000

CjAccession: A57397

R;Fukuta, M.; Uchimura, K.; Nakashima, K.; Kato, M.; Kimata, K.; Shinomura, T.; Habuchi, J. Biol. Chem. 270, 18575-18880, 1955

A;Title: Molecular cloning and expression of chick chondrocyte chondroitin 6-sulfotransf

A;Reference number: A57397

A;Recession: A57397

A;Accession: A57397

A;Accession: A57397

A;Accession: A57397

A;Accession: B57397

A;Catus: preliminary

A;Accession: B57397

A;Catus: GB:D49915; NID:G971262; PIDN:BAA08655.1; PID:G971263

C;Superfamily: chondroitin 6-sulfotransferase

C;Keywords: sulfotransferase
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A,Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A,Reference number: A96039; MUID:21368234; PMID:11474104 A;Contents: annotation C;Genetics: A,Genetics: A,Gene: SMb21237 A;Genome: plasmid
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A;Gene: COLIA1 A;Introns: 770/3; 788/3; 806/3; 842/3; 860/3; 878/3; 932/3; 968/3; 1004/3; 1022/3; 1058/ 554 GlyCys--||| | AlaAlaAlaGlnArgThrHisArgArgProFroGlyCysProArgSerAlaArgAsnPro SerGlyAlaThrProHisProGluArgGlySerGlyProAlaAspProProAlaAlaAla 352

Silica alpha 1(1) chain precursor - mouse collagen alpha 1(1) chain precursor - mouse collagen alpha 1(1) chain precursor - mouse C. Species: Mus musculus (house mouse)
C. Species: Mus musculus thouse mouse cravision 25-Apr.1997 #text change 13-Aug-1999
C. Accession: 557243 & 316374; A23802; 149557; 539789; 148300; S21626
R. Matrix Biol. 14, 593-595, 1994
Matrix Biol. 14, 594-598, 1994
Matrix Biol. 1995
Matrix Biol. 1995 ---ProArgThrTrp 659 35 ITCIGICGICITCCGIACCCAACACAATGG

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

y, Accession: 12723.

y, Status: preliminary; translated from GB/EMBL/DDBJ

y, Status: preliminary; translated from GB/EMBL/DDBJ

y, Status: DNA

y, Residues: 1-25 kRB2

y, Frestonces: GB: K01688; NID: G192246; PIDN: AAA37330.1; PID: G553881

y, Freston, S. P.; Lamande, S. R.; Hannagan, M.; Stacey, A.; Jaenisch, R.; Bateman, J.F.

y, Cochim. Biophys: Acta 1216, 469-474, 1993

A, Title: Genomic sequence of mouse COLIA1 encoding the collagen propeptides.

A, y, Reference number: S39789; MUID: 94092741; PMID: 8268229

A; Molecule type: DNA Mareidues: 1-80, 107-185;1031-1201, 'G',1203-1218, 'E',1220-1221, 'T',1223-1 Maresidues: 1-80, 'E', R.A.; Umezawa, A.; Nehls, M.; Brenner, D.A.; Breindl, M. R; Rippe, R.A.; Umezawa, A.; Nehls, M.; Brenner, D.A.; Breindl, M. Mol. Cell. Biol. 14, 5950-5960, 1994 Mol. Cell. Biol. 14, 5950-5960, 1994 Murine alpha 1(I) collagen promoter by an indirec A; Treference number: 148300; MUID:94344105; PMID:8065328 Mareing Mareing Mareing Mulliprocession: 148300

A,Status: preliminary, translated from GB/EMBL/DDBJ A,Molecule type: DNA A,Residues: 1-80,'E',82-105,'D',107-147 <REF> A,Cross-references: EMBL:X54876; NID:950486; PIDN:CAA38657.1; PID:950487

C; Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; C; Kaywords: coiled coil; extracellular matrix; glycoprotein; heterotrimer; triple helix; E; 12-2/Domain: amino-terminal propertied #status predicted <pro> F; 13-151/Domain: amino-terminal propertied #status predicted <pro> F; 13-151/Domain: amino-terminal propertied #status predicted <pro> F; 13-2-1453/Domain: amino-terminal propertied #status predicted <pro> F; 13-2-1453/Domain: amino-terminal propertied #status predicted <pro> F; 12-2-1453/Domain: collagen alpha 1(I) chain #status predicted <pro> F; 12-2-1453/Domain: fibrillar collagen carboxyl-terminal homology <pro> Alignment Scores: 0.00687</pro></pro></pro></pro></pro></pro></pro>	446 TCATG 459 GlyAl 386 CGGTG 474 326 CTGGG 266 CCAGG 266 CAGG 206 ACATG 503 ProGl 505 516 516 526 Ala
288	Collegen alpha 1(1) Chain precursor - indian (1) Alternate names: procollagen alpha 1(1) chain (1) Alternate names: procollagen alpha 1(1) chain (1) Alternate names: procollagen alpha 1(1) chain (1) Agreies: Homo sapiens (man) (2) Agreies: Homo sapiens (man) (3) Agreies: 160143; Agrass; Agrass
ArgglySerGludglyPro CAATCATGAGATCTCCTCCAGGTGCACGATAT	A;Residues: 1.369, TL, 371-589 < DAL> A;Residues: 1.369, TL, 371-589 < DAL> A;Residues: 1.369, TL, 371-589 < DAL> A;Cross-references: GB:M20789; NID:g179593; PIDN:AAB59373.1; PID:g179594 A;Cross-references: GB:M20789; NID:g179593; PIDN:AAB59373.1; PID:g179594 B;Cross-reference of a full-length cDNA clone for the prepro-alpha-1(I) chain of human A;Reference number: S01143; MUID:89025644; PMID:3178743 A;Accession: S01143 A;Molecule type: mRNA A;Residues: 1-472 < TRO> A;Cross-references: EMBL;X07884; NID:g30015; PIDN:CAA30731.1; PID:g30016; GB:M36546; NIC A;Note: submitted to the EMBL/GenBank/DDBJ databases by Prockop, D.J., 13-JUN-1988 B;Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.; Nature 310, 337-340, 1984 A;Title: Human proalpha1(I) collagen gene structure reveals evolutionary conservation of A;Reference number: A93335; MUID:84270697; PMID:646220
408 GlyProGinGlyProSerGlyProProGlyProLyBGlyAshSerGlyGlubro 425 623 TCTCCACCACCACAAGGGCTGTTGACTGCACAGGAGCCTGCAGTGAGCCGGGGGATGA 564 126 GlyAlaProGlyAsnLysGlyAspThrGlyAlaLysGlyGlubroGlyAla 442 563 TTTCATCTTGTGGGATGATGCACAGGCAGAGAGGCCCGGCTGTTCTCC 504 443	A,Residues: 1-56, Q, 60-181 <chu> A,Residues: 1-56, Q, 60-181 <chu> A,Residues: 1-56, Q, 60-181 <chu> A,Cross-references: EMBL:X00820; NII:g33657; PIDN:CAA25394.1; PID:g35658 A,Cross-references: EMBL:X00820; NII:g33657; PIDN:CAA25394.1; PID:g35658 B, Ch.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W. J. Bid. Chem. 262, 1515-15157, 1987 A,Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene ent. A,Reference number: 155254, MUID:88033098; PMID:2822714 A,Status: translation not shown; translated from GB/EMBL/DDBJ A,Residues: 1-55 <ros> A,Cross-references: GB:J02829; NID:g180387; PIDN:AAA51993.1; PID:g180388 A,Cross-references: GB:J02829; NID:g180387; PIDN:AAA51993.1; PID:g180388 R,Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gelinas, R.E.</ros></chu></chu></chu>

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A;Reference number: A35336; MUID:90252792; PMID:2339700
A;Accession: A35336
A;Molecule type: mRNA
A;Residues: 710-720, 'E',722-737,'E',739-745 <WAL>
A;Residues: 710-720, 'E',722-737,'E',739-745 <WAL>
A;Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
B;Forlino, A.; Zolezzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Mottes
Hum. Mol. Genet. 3, 2201-2206, 1994
A;Title: Severe (type III) osteogenesis imperfects due to glycine substitutions in the C
A;Reference number: I54365; MUID:95187161; PMID:7881420
A;Accession: I54365
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A;Residues: 1179-1276,'H',1278-1336,1339-1387,'R',1389-1464 <CHE>
A;Cross-references: GB:S64596; NID:g407589; PIDN:AAB27856.1; PID:g407590
A;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBIP:136445)
A;Note: does not represent an experimentally determined sequence but three different mut
A;Accession: B47426
A;Reference number: S15989; MUID:90326017; PMID:2374517
A;Accession: S15989
A;Accession: S15989
A;Moldcule type: mRNA
A;Moldcule type: mRNA
A;Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 <LAB>
B;Wirtz, M.K.; Rao, V.H.; Glanville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N
Connect: Tissue Res. 29, 1-11, 1993
A;Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of A;Reference number: 152905; MUID:93339042; PMID:8339541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 342-352, C' 354-359 <WI2>
A;Residues: 342-352, C' 354-359 <WI2>
A;Cross-references: GB:864717; NID:940B195; PIDN:AAB27677.1; PID:940B196
A;Note: mutant sequence from patient with osteogenesis imperfecta
R;Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Bikenberry, B.F.; Prockop, D.J.
Bjochemistry 22, 5213-5223, 1981
A;Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalphal
A;Reference number: A90476; MUID:84080385; PMID:6689127
A;Accession: A90476
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A,Residues: 425-1250, X7,1252-1328, S7,1330-1390, X7,1392-1464 <BER>
A,Residues: 425-1250, X7,1252-1328, S7,1330-1390, X7,51395-14
A;Cross reference partially completed for missing nucleotides by A29439
R;Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
D. Biol. Chem. 260, 691-694, 1985
A;Title: Multiaxon deletion in an osteogenesis imperfecta variant with increased 'A,Reference number: A22161; MUID:85104934; PMID:2981843
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A;Molecule type: DNA
A;Residues: 746-766,'8',768-781 <POR>
A;Residues: 746-766,'8',768-781 <POR>
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A;Cross-references: GB:L47667; NID:g1009093; PIDN:AABS9576.1; PID:g1009094
B;Chessler, S.D.; Wallis, G.A.; Byers, P.H.
J. Biol. Chem. 268, 18218-18225, 1993
J-Fitle: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(1
A;Reference number: A47426; WUID:93352646; PMID:8349697
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Residues: 1179-1464 - CCH4>
Experimental source: normal dermal fibroblast culture
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A,Residues: 1179-1336,1339-1464 <CH6>
A,Experimental source: fetal cell 86-146
A,Accession: E47426
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Residues: 1179-1276,'H',1278-1464 <CH5
Experimental source: fetal cell 86-237
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AyAccession: S09400
AyAccession: S09400
AyRolecule type: mRNA
AyResidues: 156-183 <WEI>
RyClick, E.M.; Bornsterin, P.
ByCochemistry 9, 4699-4706, 1970
AyItile: Isolation and characterization of the cyanogen bromide peptides from the alphal
AyReference number: A90567; MUID: 71038625; PMID: 5529814
AyAccession: B90567
AyAccession: B90567
AyAccession: B90567
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AyResidues: 162-198, 'Z', 200-201, 'Z', 203-206, 'Z', 208-209, 'Z', 211-228, 'B', 230, 'BB', 233, 'Z'
AyRecession: Bochem: 192, 153-159, 1990
AyRete evidence for 170-allysine
RyBeatege, B; Notbohu, H; Diebold, J; Lehmann, H; Bodo, M; Deutzmann, R; Mueller, E.
Eur. J. Biochem: 192, 153-159, 1990
AyRetes and anumber: S1372; MuID: 90382436; PMID: 2169412
AyAccession: S1372
AyMolecule type: protein
AyAccession: S1372
AyAccessi
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 258-268:1347-1357 <DEA>
A;Residues: 258-268:1347-1357 <DEA>
A;Cross-references: GB:S67495; NID:9239007; PIDN:AAB20350.1; PID:9239008
A;Notes sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report R;Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
B;Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
A;Title: Comparative study of glycopeptides derived from selected vertebrate collagens.
A;Reference number: A92069; MJID:71001508; PMID:4319110
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A, Residues: 1-34 <-R25
A, Residues: 1-34 <-R35
A, Creating to the control of the control
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Title: A base substitution in the exon of a collagen gene causes alternative splicing Reference number: S09400; MUID:89356643; PMID:2767050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:J03559; NID:g180876; PIDN:AAA52052.1; PID:g553238
R;Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.
J. Biol. Chem. 260, 2315-2320, 1985
A;Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter A;Reference number: I55237; MUID:85130970; PMID:2857713
                                                      coc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987
Title: Regulatory elements in the first intron contribute to transcriptional control Reference number: A39943; MUID:88097389; PMID:3480516
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5-hydroxylysine
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A;Note: attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose
R;Labhard, N.E.; Hollister; D.W.
Matrix 10, 124-130, 1990
A;Title: Segmental amplification of the entire helical and tel
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A.Status: translation not shown; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
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A;Residues: 263-268 <MOR>
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Residues: 33-52 <WIR>
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the complete human thrombospondin 2 cDNA: pote: PMID:8406456
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A)Gene: GDB:THBB2; TSP2
A)Cross-references: GDB:128789; OMIM:188061
A)Map position: 6427-6427
C)Complex: homotrimer, disulfide linked
C;Function:
A)Description: participates in cell migration and adhesion, and in platelet aggregation
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C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 13-Aug-1999
C;Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 13-Aug-1999
C;Accession: A47379; A42173
R;Labell, T.L.; Byers, P.H.
Genomics 17, 225-229, 1993
A;Title: Sequence and characterization of the complete human thrombospondin 2 cDl
A;Reference number: A47379; MUID:94010892; PMID:8406456
A;Accession: A47379
A;Molecule type: mRNA
A;Residues: 1-112 cALBA
A;Residues: 1-113 
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   333 ProProGlyProThrGlyProAlaGly------ProProGlyPheProGly-Al 348
                                                                                                                       ---LysGlyGluAlaGlyProGlnGlyProAr 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 GCTCGGGCTGTGCCTTCATAGACAGGGAGCTGATGTTGTGGCTGTACATGTGGAAATA
                                                                TGTAGGAGGGGCAGGCCTTCTCCACCACCTCAAAGGGCTGTTGACTGCACAGGAGCCTGC
                                                                                                                                                                                                                                            --GlnGlyvalArgĠiyGluProGlyProPr
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                                                                                                                                                                                     GGGCCCGGCTGTTCTCCCACTGAAAGAGGCTGGACTG-----TCTCCGGGGACCAGGTT
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                                                                                                                              348 aValGlyAla-
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A; Molecule type: mRNA
A; Residues: 1179-1387, 78, 1389-1464 < CH7>
A; Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; Nić
J. Biol. Chem. 263, 14605-14607, 1988
A; Reference number: 155269; MUID:89008319; PMID:3170557
A; Accession: 155269
A; Accession: 155269
A; Accession: 155269
A; Residues: 1187-1194, C., 1196-1220
A; Residues: 1187-1194, C., 1196-1220
A; Residues: 1187-1194, C., 1196-1220
A; Note: mutant sequence from a patient with mild osteogenesis imperfects
A; Note: mutant sequence from a patient with mild osteogenesis imperfects
A; Note: mutant sequence from a patient with mild osteogenesis imperfects
A; Note: mutant pro-alpha-1(1) collagen: CDNA sequence for the C-propeptide domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315 AlaProGlyProAlaGlyAlaArg-----GlyAsnAspGlyAlaThrGlyAlaAlaGly 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----AGAGGGACTGCAGGTTGAAGAAGCGCACCTCCTTGAGCACCACGTGGC 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 GlyProProGlyProProGlyLeuGlyGlyAsnPheAlaProGlnLeuSerTyrGlyTyr 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GAGCCAGGTCCTCATAGCGCACAA--- 945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 ProProGlyGluProGlyGluProGlyAlaSerGlyProMetGlyPro----- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------ArgGlyProProGlyProFroGlyLysAsnGlyAspAspGlyGluAla 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCAGATGACCTGCATCACATAGTAGGGTTGGTCCTCCTTCTTGAGTTTTTGCTCATGCT 819
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C;Superfamily: thrombospondin 1; EGF homology; thrombospondin type 1 repeat homology; vd C;Keywords: beta-hydroxyasparagine; calcium binding; cell adhesion; glycoprotein; Fil-18/Domain: signal sequence #status predicted <sig> F;19-172/Product: thrombospondin 2 #status predicted <mat> F;19-377/Domain: von Willebrand factor type C repeat homology <vwc> F;380-431/Domain: thrombospondin type 1 repeat homology <thr1> F;43-549/Domain: thrombospondin type 1 repeat homology <thr2> F;53-589/Domain: EGF homology <egf> F;552-561/Domain: EGF homology <egf> F;526-561/Domain: EGF homology <egf> F;552-561/Domain: EGF homology <egf> F;552-561/Domai</egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></egf></thr2></thr1></vwc></mat></sig>	Alignment Scores: 0.0121 Length: 1172 Pred. No.: 143.50 Matches: 131 Score: 133.50 Matches: 131 Percent Similarity: 29.09\$ Conservative: 61 Best Local Similarity: 19.85\$ Mismatches: 229 Query Match: 19.85\$ Indels: 239 DB: 1 (1-2043) x TSHUP2 (1-1172)	Qy 199 CCACATGTACAGCCACAACATCAGCTCCCTGTCTATGAAGGCACAGCCCCAG 250	Db 267 uArgSerCysGluGluLeuGlyAsnMetValGlnGluLeuSerGlyLeuHisValleuVa 287 Cy 268 TCTGTCTTCCTGGGGGTCTTTTTTTTGTGGGGGAGGT 309 Db 287 lAsnGlnLeuSerGluAsnLeuLySArgValSerAsnAspAsnGlnPheLeuTrpGluLe 307	OY 310 ITTTGGGCAGCACCCAGATGTTTCTACCTGATGGAGCCCGCCTGGCACGTGTGGATGAC 369	326 ePheAlaGluAshGruTrpValValAspSerCy 430 CTTCTTGTGGGACATGAGGGTCTTTGATGCCTACATGGAACCTGGTCCCCGGAGACAGTC	Db 338 sThrThrCysThrCysLysLysPhe	ACAAG CAGTC	Db 373 erCysLeuHisSerValAspGlyGluGluGlyTrpSerProTrpA 388 Qy 643 CCACGTGGTGCTCAAGGAGGGCGTTCTTCAACCTGCAGTCCTCTTCCACCTCTCTCCACCTCTTCTCAACTGCTGCT 696 Db 388 laGluTrpThrGlnCysSerValThrCysGlySerGlyThrGlnGlnArgGsrC 408	Qy 697 GCTGAAAGACCCCTCCTCAACCTGCATATCGTGCACC- 734	427 euSerLysCysAspThrArglleArgGlnAspGlyGlyTrpSerHisTrpSerPr

ζ	1684 AGCATTTTCCACAGAG 1699	Db 842 GlyProThrGlySerSerGlyProAlaGlyProProGlyProGlnGlyValLys 859
QD	11: ::: ::: 736 eGlyAspAspAspAspAspAspAspAspAspAspAspAspAspA	CTTGTAGATCTCCAGCT 88
Š	1700 -AIGCGAAITCIGAGCCCTIGGAGTTCCCAAIGGGATTCAAGGAAGIGGGAACAAG 1758	
Dp	756 sGlnLeuLeuPheAsnProArgGlnAlaAspTyrAspLysAspGluValGlyAspAr 775	IGAGTT
δλ	1759 GTIGGAJGCCTACTTATGAGCTIGACCATACAGCTATCGGTAATCAGAAATA 1810	
qq	775 gCysAspAsnCysProTyrValHisAsnProAlaGln1le 788	830 TTTGCTCATGCTGCCCATCACAATGCGACTGTCAATCAT
RESULT 1	10	proserglyAlaProglyLys
collagen	n alpha 1(III) chain precursor - mouse	
C; Date:	10-Apr-1996 #sequence revision 19-Apr-1996 #text_change 13-Aug-1999	IaG⊥y
C; Access R; Toman,		
Gene 147	Gene 147, 161-168, 1994 A:Title: The mouse type-III procollagen-encoding gene: genomic cloning and complete DNA	
A; Rerere A; Access A; Molecu	A;kdrerence number: Sisyaso; Mullissullous; FMIL:/szo/si A;Accesion: SisyaSo A;Accieule type: DNA	
A; Residu	A;Residues: 1-1464 <icm></icm>	
A;Cross-: R;Toman,		Qy 653 GCACCACGTGGCTGTAGGAGCGCCCTTCTCCACCACCTCAAAGGGCTGTTGACTGC 594
Submitte A.Refere	submitted to the EMBL Data Library, November 1994 A:Reference number: S62120	Db 960ProProGlyMetProGlyProArgGlySerProGlyProGlnGly1le 975
A; Access	AACCESSION: S62120	TGTGGGATGATGT
A; Residu	NA - CAA3627	916
R; Metsa(, Vuorio, E.	OV 533 GTGCAGAACACAGGGCCCGGCTGTTCTCCCACTGAAAGAGGCTGGACTGTCTCCGGGGAC 474
A;Title	. Blophys. Acca 1003, 441-243, 1531 : Specific hybridization probes for mouse type I, II, III and IX collagen mRNAs.	066
A; Acces:	ence number: Stelle, note: preference stellers and stellers are stellers are stellers and stellers are stellers and stellers are stellers are stellers and stellers are stelle	473
A; Molect	s: pretuninaly use: 1442-1444 AMET.	1005
A; Cross	des: Int. 173 (121) - Pibrichences: EMBL:X57983; NID:g50476; PIDN:CAA41048.1; PID:g50477	413
A; Intro	C.Generacs.s. A.Introns. 29/1; 95/3; 112/3; 150/3; 175/3; 193/3; 211/3; 229/3; 247/3; 265/3; 283/3; 29 58/3. 573/3. 706/3: 742/3. 760/3: 778/3: 746/3: 814/3: 850/3: 868/3: 886/3; 940/3; 976/3	1022
C;Super	lar collagen carboxyl-terminal	Oy 353 AGGCGGCTCCATCAGGTAGAAACATCTGGGTGCTGCCCCAAAAAGCTGCCCCAAAAG 294
F;1-24/ F:25-15	Domain: Signal Bequence #status predicted <sig> 4/Domain: bropeptide #status predicted <pro></pro></sig>	Db 1039 odlyhlaproGlyAlaProGlyHisProGlyProProGlyProValGlyProSerGly 1058
F,32-92	F;32-92/bomain: von Willebrand factor type C repeat homology <vwc> F;32-92/bomain: collagen alpha 1(III) chain #status predicted <mai> F;155-1464/Product: collagen alpha 1(III) chain #status predicted <mai></mai></mai></vwc>	CY 293 AAGAGCCAGAGCGCAGGAAGACAGAAGACCAGCGTGCGTG
F;1236-	1464/DOMAIN: IIDIILLAI COLLAGEN CAIDOXYI-CEIMINAI NOMOLOGY SICCO	
Alignment Pred. No.:	Scores: 0.0213 Length:	174
Score: Percent	Marches: Conservative:	Db 1070GlyProSer 1072
Best Local S Query Match: DB:	cal Similarity: 27.11% Mismacches: 130 3.80% Indels: 106 2 Gaps: 20	Qy 173 GGGAAACCAGAAACAGCAGGAGCT 150
US-09-645	45-078-1 (1-2043) x S59856 (1-1464)	SULT 11
ò	1124 CCTGGGAGACATTAAAGGGCATCCTGGCATTTGTGTGGAAAGCGTGGTCACCCATGCCCT 1065	JB0291 FB19 protein - human
QQ	814 ProglyginasnGlyglubroGlyglaLysGlyGluArgGlyglaBro 829	C;Species: Homo sapiens (man) C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
È		C,Accession: JE0291 R;Totaro, A.; Griffa, A.; Carella, M.; Rommens, J.M.; Valentino, M.A.; Roetto, A.; Zelant
ДQ		Biochem. Biophys. Kes. Commun. 250, 555-557, 2556 A.Title: Cloning of a new gene (FB19) Within HLA class I region.
ò	1004 ATTCATAGATTCGGGAAAGTCTGGGCCACAGGGGCTCGAGGCCAGGTCCTCATAGCGCACAA 945	A;kererence number: JEUZ91; MUID:990U3*93; FMID:9/04501. A;Accession: JE0291

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TGAGGGAGGGGTCTTTCAGCAGCGGTAGAGGGACTGCAGGTTGAAGA----AGCGCACCT
284 AGCGCCAGGAAGACAGAACCAGCACGTGCATGCGCTC
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Best Local Similarity:
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|GlyproGlyGlyProLysGlyMetGlnHisPheProProGlyProGlyGlyProMetPro
                                                                                                                                                                                                                                                                                           TCTTGTAGATCTCCAGCTGGCTTTGGCAGATGACCTGCATCACATAGTAGGGTTGGTCCT
       A,Molecule type: mRNA
A,Residues: 1-940 <TOT>
A,Cross-references: GB:Y13247; NID:g2117158; PIDN:CAA73697.1; PID:g2117159
C,Genetics:
A,Gene: FB19
A,Map position: 6p21.3
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820 yGlyGlyMetGlyAlaGlyGlyGlyHisArg-----
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A43291
collagen alpha 2(I) chain precursor - mouse
collagen musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
C;Date: 10-Sep-1999 #sequence revision 20-Sep-1999
A;Reference number: A4329; MUD:92372043; PMID:1505972
A;Residues: 1-1373 <PHI>A;Residues: 1-1373 <PHI>A;Residues: 1-1373 <PHI>A;Residues: 1-1373 <PHI>A;Residues: 1-1373 <PHI>A;Residues: 1-1373 <PHI>A;Residues: 1-1373 <PHI
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A;Residues: 1-1273 <PHI
A;Reference number: A54328; MuID:92084969; PMID:1748823
A;Reference number: A54328; MuID:92084969; PMID:1748823
A;Residues: 1-110 <PHI>A;Residues: 1-110 <PHI
A;Residues: 1-110
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us-09-645-078-1.rpr

GlyaladlaGly 607 A;Residues: 1-28,'R',99-1487 <su2> A;Residues: 1-28,'R',99-1487 <su2> A;Residues: 1-28,'R',99-1487 <su2> A;Residues: BMB1.X16468) NID:g29515; PIDN:CAB34488.1; PID:g29516 A;Note: alternative splice form 1 B;Vikkula, M.; Metsaeranta, M.; Syvaenen, A.C.; Ala-Kokko, L.; Vuorio, E.; Peltonen, L. Biochem, J. 286, 287-294, 1992 A;Title: Structural analysis of the regulatory elements of the type-II procollagen gene A;Reference number: S24270; MUID:92344585; PMID:1637314 A;Reference number: S24270; MUID:92344585; PMID:1335559 A;Note: this translation is not annotated in GenBank entry HSPROCOEI, release 111.0 B;Rochest 1-18, 1986 A;Reference number: A24828; MUID:87031574; PMID:3021582 A;Reference number: A24828; MUID:87031574; PMID:3021582</su2></su2></su2>	381 693 345 713 321 733	753 214 764 764 154 781 97	stThrd1 793	Splice form 1; collagen A; Residues: 171-172, C', 174-175 cALA> Note: mutant sequence from a family with family with primary generalized osteoarthrit; Note: mutant sequence from a family with family with primary generalized osteoarthrit; Note: mutant sequence from a family with family with primary generalized osteoarthrit; Note: mutant sequence from a family with family with primary generalized osteoarthrit; Note: Collagen type: Tx from human cartilage: a structural profile of intermolecular collagen type in protein. Note: Collagen type: Note: Null: N
	440 CGCACAAGAAGACGGCCCGTATCAGATCCCGCACAGCCATGTGCAGCATCCAGGGGGTGC 674 nThrGlyArgAspGlyAlaArgGlyIleProGlyAla	733 yProAlaGlyAlaAlaGlyGlnProGlyAlaLyGGlyGluLysGlyThrLysGlyProLy 273 GACAGAACCAGCACGTGCATGGCTGGCTGTGCCTTCATAGACAGGGAGCTGTTG 753 SGlyGluAsnGlyIleValGlyProThrGlySer 213 TGGCTGTACATGTGGAAATAGAGCCAAGATGATGTGTGTG		te names: procollagen alpha i(II) chain s: chondrocalcin; collagen alpha i(II) chain precursor s: Homo calcin; collagen alpha i(II) chain precursor s: Homo calcin; collagen alpha i(II) chain precursor con: Assis; collagen alpha i(II) chain precursor con: Assis; sof715; 52470; A24828; Sof496; A35428; A30 for: Assis; Sof715; 52470; A24828; Sof496; A35428; A30 for: Assis; M.; Sandell, L.J. The human type II procollagen gene: identification of a noe number: A38513; MUD:91184811; PMD:2081599 for: A38513 for: A

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', Molecule type: DNA
', Residues: 1266-1388 cMUN2>
', Residues: 1266-1388 cMUN2>
', Residues: 1266-1388 cMUN2>
', Rossidues: 1266-1388 cMUN2>
', Rossidues: DNA
', Rossidues:
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Residues: 7-28;'R',99-114;541-578;786-802;1055-1056,'N',1058-1068,'T',1070-1109;1200-1
Accession: 184453
                                                                                         .Cross-references: EMBL:X00339; EMBL:X00298; NID:g394699; PIDN:CAA25092.1; PID:g4378975
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A;Residues: 541-560 <SAN3>
A;Cross:references: EMBL:X02378; GB:M23870; NID:g30107; PIDN:CAA26227.1; PID:g929621
A;Acoession: 137251
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Molecule type: DNA;
Residues: 7-28 <SAN2>
)Cress-references: GB:M23759; NID:g180845; EMBL:X03320; GB:M24938; NID:g30104;
)Acression: 137250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .085 AAGCGTGGTCACCCATGCCCTTGCCTCGGGTGATGTTATGCACCCAGGTCTGAAGATGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----ArgGlyProProAspProGlnGly
                                                                                                                                                           A,Molecule type: DNA
A,Residues: 894-909, PE' <STR2>
A,Cross-references: G8:K01785; NID:g30035; PIDN:CAA25082.1; PID:g1335032
A,Cross-references: G8:K01785; NID:g30035; PIDN:CAA25082.1; PID:g1335032
R;Nunez, A.M.; Francomano, C.; Young, M.F.; Martin, G.R.; Yamada, Y.
Biochemistry 24, 6343-6348, 1985
A,Title: Isolation and partial characterization of genomic clones coding
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Reference number: A24561; MUID:86104139; PMID:3002437
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138.50
35.47%
29.39%
                                                         Residues: 1245-1295 <STR1>
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A; Residues: 1032-1056, Nr, 1058-1068, Tr,,1070-1487 cCHE>
A; Cross-references: GB:J00116; NID:g180395; PIDN:AAA51997.1; PID:g180396
A; Cross-references: GB:J00116; NID:g180395; PIDN:AAA51997.1; PID:g180396
B; Elima, K.; Vucrio, T.; Vucrio, Vucrio, T.; Vucrio, Vucrio, T.; Vucrio, Vucrio, T.; Vucrio, Vucrio, T.; Vucrio, Vucrio, T.; Vucrio, Vucrio, T.; Vucrio, Vucrio, T.; Vucri
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, Residues: 1164-1184, GPSGKDGANGIPGPI',1185-1199 <TIL2>
, Gross-references: EMBL:N37126; NID:9180808; PIDN:AA55037.1; PID:9180809
, Gross-references: EMBL:N37126; NID:9180808; PIDN:AA55037.1; PID:9180809
, Cheath, K.S.E.; Stoker, N.G.; Griffin, J.R.; Grosveld, F.G.; Solomon, E.
roc. Natl. Acad. Sci. U.S.A. 82, 2555-2559, 1985
, Title: Identification and characterization of the human type II collagen gene (COL2A1)
, Reference number: A02858; MUID:85190534; PMID:3857598
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Aesidues: 1032-1056, N/,1058-1068, T/,1070-1487 <CHE>
COMBOURDES: 1032-1056, N/,1058-1068, T/,1070-1487 <CHE>
COMBOURDES: 1032-1056, N/,1058-1069, DIDN:AAA51997.1; PID:g180396
AEIma, K.; Vuorio, T.; Vuorio, E.
Unleic Acids Res. 15, 9499-9504, 1987
AITICE: Determination of the single polyadenylation site of the human px
Reference number: A27280; MUID:88067771; PMID:2825137
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Db 92 ArgValArgAspArgAspArgAsrCysSerProSerArgArgCysTrpGly 108 Qy 306 AGCTTTTGGGCAGCACCCAGATGTTTTCTACCTGATGGAGCCGCACGTGTGCA 365 Db 109TrpProSerLygGlyCysArg 115 Qy 366 TGACCTTCAAGCAGAGCACCGCTGGATrpProSerLygGlyCysArg 115 Db 116ProGlyLysArgGlyGlyAlaGlyArpProArgArgSerLygThrTrpCys 134 Qy 396 TGCACATGCCTGTGGGAATCTGATACGGGCGTCTTCTTGTGCGACATGAGCGTCTTTG 455 Db 135 GlyGlyTrpArgAlaAlaSerThrSerGlySerSerCysAlaAlaArgArgLysArgArg 154 Qy 456 ATGCCTACATGGAACCTGGTCCCGGAGACAGCCGCTCTTTCAGTGGAAACAGCC 515 Db 155 ArgArgHisTrpGlySerSerGlyProSerSerGlyCysSerAla 169 Qy 516 GGGCCCTGTGTTCTGCACTGCTGCTGTACCAAGATGAAATCATCCCCC 572 Qy 516 GGGCCCTGTGTTCTGCACTGTGAACATCATCCCCC 572 Db 170 AsnThrThrArgAlaArgHisAlaProAlaArgSerSerPro 183	QY 573 GGGCTGAGGGCTCCTGTGCAGACAGCCCTTTGAGGTGGTGGAGAAGG 626. Db 184 LeualaSerThrGlyHisSerProhlaalaSerGlyTrpGlyArg198 QY 627 CCTGCGGCTCTACAGCCACGTGGTGCTCAAGGAGGTGCGCTTCTTCAACTGC 680 Db 199SerProSerArgAsnTrpCysGlyAlaAlaArgProSerValSerSerGlyArg 216 QY 681 AGTCCTCTACCGGTGCTGTAAAGACCCTCCCTCA 716 Db 217 AlaThrSerThrArgCySTrpProAlaAlaSerAlaAsnSerValProLysProProSer 236 Qy 717 ACCTGCATATGG	Db 237 SerProArgSerValArgAlaGlyThrArgTrpGlyCysCysThrTrpThrPro 254 Qy 750 GGGCCGTGTTCCCGAGAACGCACAAAGGGAGATCTCATGATGACATTG 809 Db 255 GlyAlaProAlaAlaProArg	SIL INCOMPTIONING STATE 15 RIIS Liagen alpha 1(1) chain - re Species: Rattus norvegicus (Bornstein, P. 1981 #sequence Bornstein, P. 63-71, 1965; A Bornstein, P. 63-71, 1967; A Softense: Comparative sequence Reference number: A90559; M Accession: A90559 Molecule type: protein Residues: 1-19 aB01. Experimental source: tendon
Db 516 GlyPheProGlyGlnAspGlyLeuAlaGlyProLysGlyAlaProGlyGluArgGlyPro 535 Qy 797 CAATCATGAGATCTCCCTTTGTGCGTTCTCGGGAACGGAACGGGCCGGGGGTCCCGGA 738 Db 536 SetGlyLeuAlaGlyProLysGlyAlaAspGlyArgProGlyArgProGlyGlyBroGly 555 Qy 737CCAGGTGACGATATGCAGGTTGAGGGAGGGGTCTTTCAGCAGCGGGTAGAGGGAC 681 Db 556 LeuProGlyAlaArgGlyLeuThrGlyArgProGlyAspGaGCTCTT 621 Db 556 LeuProGlyAlaArgGlyLeuThrGlyArgProGlyAspGaGCCTGTG 621 CAGGTTGAAGAGCGCACCTCTTGAGCACACGTGGCTGTAGGAGCGCTTCT 621 Db 575 ValGlyProSerGlyAlaProGly	503 ACTGA 619 Glu-L 443 TGTCG 637 uThrG 395 GCATC 657 YAlaP	hypothetical protein - Deinococcus radiodurans (strain R1) hypothetical protein - Deinococcus radiodurans (strain R1) c;Species: Deinococcus radiodurans c;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000 C;Accession: F75420 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma; Siente, M.; Venter, J.C.; Fraser, C.M. S; Smith, H.O.; Venter, J.C.; Fraser, C.M. S; Smith, H.O.; Venter, J.C.; Fraser, C.M. A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036996; PMID:10567266 A;Accession: F75420 A;Accession: F75420 A;Residues: 1-319 <-WHI>A;Residues: 1-319 <-WHI>A;Residues: 1-319 <-WHI>A;Cross-references: GB:AE001971; GB:AE000513; NID:g6458972; PIDN:AAF10810.1; PID:g645898 A;Experimental source: strain R1 C;Genetics: A;Gene: DR:229 A;Map position: 1	Alignment Scores:

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A. Accession: Wellse A. Molecule type: protein a Molecule type: protein a Molecule type: protein the composition of peptides comprising residues 1-9 and 1-19 confirms the sequench A. Mote: the composition of peptides at the third position of the tripeptide repeating unit (and subsequently O-glycosylated.

A. Mote: the complete chain contains 1052 residues.

C. Comment: The complete chain contains 1052 residues.

C. Superfamily: collagen alpha 1(1) chain, fibrillar collagen carboxyl terminal homology;

C. Modified site: blocked amino end (Glx) (probably pyrrolidone carboxyl caid) #status F; 103, 424, 547/Binding site: allysine (Lys) #status experimental

F; 103, 424, 547/Modified site: brydroxylysine (Lys) (covalent) #status experimental

F; 124, 547/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
                        to positions 949-1032 of the alpha 1(I) chain (of neutral salt-extracted rat skin collagen) in:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 ArgGlyArgProGlyProProGlySerAlaGlyAlaArgGlyAspAspGlyAlaValGly 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- CCTTCTTGAGTTTTTGCTCATGCTGCCCCATCACAATGCGACTGTCAATCATGAGAT 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---problaglybladlyProblaglyBsnProdiyAlaAspGlyGlnProdlyAla 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pheproGlyAlaAlaGlyAlaLysGlyGluAlaGlyProGlnGlyAlaArgGlySerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     785 CTCCCTTTGTGCGTTCTCGGGAACGGAACACGGCCCGGGGGTCCCGGA---CCAGGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 941 GGTAGCGTTCCTGCAGGGCCTTGGGCAAGGACTGGATGGTCTTGTAGATCTCCAGCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1144 GGGCAAAGACCAGCGCCAAGCCTGGGAGACATTAAGGGCATCCCTGGCAT--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1067 CCTTGCCTCGGGTGATGTTATGCACCCAGGTCTGAAGATGGGGCA---
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                                     A,Note: this region probably corresponds to positions 949-87, Note: the major antigenic determinant (of neutral salt-e. R;Stoltz, M.; Timpl, R.; Kuehn, K. FEBS Lett. 26, 61-65, 1972
FFBS Lett. 26, Non-helical regions in rat collagen alphal-chain. A;FeFerence number: A91385; MUID:73049495; PMID:4636751
A;Contents: CNBr6
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A;Note: sequences from skin and tendon appear to be identical
A;Note: the amino-terminal tetrapeptide may be removed by limited proteolysis during ext
R;Kang, A.H.; Bornstein, P.; Piez, K.A.
Biochemistry 6, 788-795, 1967
A;Title: The amino acid sequence of peptides from the cross-linking region of rat skin of A;Reference number: A90552; MUID:67162268; PMID:5337886
A;Contents: CNBY1
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A, Molecule type: protein
A, Residues: 419-677 < 8013.
A, Essidues: 419-677 < 8013.
A, Experimental source: skin
R, Stoltz, M.; Timpl, R.; Furthmayr, H.; Kuehn, K.
Eur. J. Biochem. 37, 287-294, 1973
Eur. J. Biochem. 37, 287-294, 1973
A, Title: Structural and immunogenic properties of a major antigenic determinant in IA, Reference number: A91209, MUID:74011954; PMID:4126850
A, Contents: CNBr6
A, Accession: A91209
A, Molecule type: protein
A, Residues: 568-651 < 511>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 242, 2572-2574, 1967
A,Title: The incomplete hydroxylation of individual prolyl residues in collagen. A,Reference number: A92029; MUID:67165368; PMID:4290711
A,Contents: CNBr2
A,Accession: A92029
                                                                                                                                                                                                                                                                                                                          A,Molecule type: protein
A,Readues: 5-19 «KAN»
A,Experimental source: skin
K,Bornstein, P
J. Biol. Chem. 242, 2572-257
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us-09-645-078-1.rpr

:::	683 ACTGCAGGTTGAAGAAGCGCACCTTGAGCACCACGTGGCTGT 639	255 ProSerGlyProGlnGlyProSerGlyAlaProGlyProLysGly 269	638 AGGAGGGGCGTTCTCCCACCTCAAAGGGCTGTTGACTGCACAGGAGCCTGCAGT 579	270 AsnSerGlyGluProGlyAlaProGlyAsnLysGlyAspThrGlyAlaLysGly 287	578 GAGCCCGGGGGATGATTTCATCTTGTGGGATGATGTCACAGGCAGG	288 GlubroGlyGly 296	518 CCCGGCTGTTCTCCCCACTGAAAGAGGCTGGACTGTCTCCGGGGGACCAGGTTCCATGTAGG 459	297 ProproglyProAlaGlyGluGluGluGlyP305	458 CATCAAAGACGCTCATGTCGCACAAGAAGACGGCCCGTATCAGATCCCGCACAGCCATGT 399	306LysArgGlyAlaArgGlyGluProGlyProSerGlyLeuFroGlyProFro 322	398 GCAGCATCCAGGCGGTGCTCTGCTTGAAGGTCATCCACACGTGCCAAGCGGGGCTCCATCA 339	323GlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	338 GGTAGAAAACATCTGGGTGCTGCCCAAAAAGCTGCCCCAAAAAAAA	330 SerArgGlyPheProGlyAlaAspGlyValAlaGlyProLysGlyProAlaGly 347	278 AGGAAGACAGAACCACGTGCATGCGCTCGGGCTGTGCCTTCATAGACAGGGAGCTGA 219	348 GluargGlySerProGly353	218 IGTIGIGGCIGTACAIGIGGAAGAATAGAGCCAAGAIGGCCATGGCAAACCAGAAACA	354354	158 GCAGGAGCTTCATTTTTAGGCAGTAGCATTGTGCTGAAGTGGAAGACCTTGTGGCTTG 99	364 AlaGlyArgProGlyGluAla 370	98 GGCTTCCTGCTGCTTTTGAGAGGCTCACTGCTAGCCGGCCATGCGCTTTTCTCTTA 39	371 GlyLeuProGlyAlaLysGlyLeuThrGlySerProGlySerProGly 386	38 CCC 36	387 Pro 387	
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Search completed: May 6, 2004, 11:07:20 Job time : 63.5 secs

Scoring table:

Minimum DB Maximum DB

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score:

Title: Perfect

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Sequence:

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                   P11391 rattus norver 993466 home sapien 003376 chirconowus 299466 home sapien 299466 home sapien 2014162 home sapien 2014162 home sapien 2014162 home sapien 2014163 home sapien 2014163 home sapien 201416 mus musculu 20148 musculu 20148 mus musculu 20148 musculu 20
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homo sapien
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-!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Q02388
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STRAIN=White leghorn; TISSUE=Embryonic chondrocytes;
MEDLINE-95355490; PubMed=7629189;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-11997 (Rel. 35, Last annotation update)
Gallus gallus (Chicken).
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CC07 CAEEL
IF2 COREF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA1A HUMAN
CA21 HUMAN
CA13 HUMAN
IF2 STRCO
NTC3 MOUSE
                                                                         CA21_RAT
CA21_RANCA
CA17_HUMAN
CA21_BOVIN
                                                                                                                                                                                                                 NTC4 HUMAN
BAR3 CHITE
NTC4 HUMAN
HCN4 RABIT
CA21 CHICK
SREC HUMAN
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Gallus.
NCBI_TaxID=9031;
similarity)
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C6ST_CHICK
     Command line parameters:
-MODEL=frame+ n2p.model - DEV=Xlp
-MODEL=frame+ n2p.model - DEV=Xlp
-MODEL=frame+ n2p.model - DEV=Xlp
-Q=/cgn2_1/USFPC_Spool_p/US09645078/runat_06052004_104559_21727/app_query.fasta_1.2183
-DES-WissPrct 42 - QFMT=fastan - SUFFIX=rsp - MINMATGH=0.1 - TOOPCL=0 - LOOPEXT=0
-UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-UNITS=bits - START=1 - END=-1 - MATRIX=100 - TRANS=human40.cdi - LIST=45
-UNITS=bits - START=1 - END=-1 - MATRIX=100 - TRANS=Numan40.cdi - LIST=45
-UNITS=bits - START=1 - END=-1 - MATRIX=100 - TRANS=12 - NODEL=0.15 - NODEL=0.3
-USER=US09645078 @CGN 11 1 22 @runat - 06052004 104559 21727 - NCPU=6 - ICPU=3
-NO WARA - LARREQUERY - NGG SCORES=0 - MAIT - DSPBANCK=100 - LONGLOG
-DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - XGAPEXT=0.5 - FGAPOP=6
-FGAPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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                                                                                                                                          frame_plus_n2p model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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PIR; A57397; A57397. InterPro; IPR000863; Sulfotransferase. Pfam; PF00685; Sulfotransfer; 1. Transferase; Transmembrane; Signal-anchor; Glycoprotein; Golgi stack.

EMBL; D49915; BAA08655.1; -.

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| ProLeuTrpHisIleGluArgThrValThrPheGluProGlyGlyAlaAsnAlaValGly
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SerSerHisSerLeuCysGluGluProValCys----ThrProSerLeuLysLysVal
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LeuGlnGluAspGlu---ValGlnArgLeuArgGlyAsnCysGluSerIleArgLeuSer
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CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
                         LUMENAL, CATALYTIC (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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MEDLINE=84270667; PubMed=6087149;
Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
Baer T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
Tuffnell P.S., Barrell B.G.,
"DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
Nature 310:207-211(1984).
                                      350 TyrGluAspValAlaArgAlaProLeuArgLysAlaLeuGluMetTyrArgPheAlaGly
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TATGAGGACCTGGCTCGAGCCCCTGTGGCCCCAGACTTCCCGAATGTATGAATTCGTGGGA
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1988 (Rel. 01, Last annotation update)
Hypothetical BHLF1 protein.
Epstein-barr virus (strain B95-8) (Human herpesvirus
Viruses; daDNA viruses; no RNA stage; Herpesviridae;
dammaherpesvirinae; Lymphocryptovirus.
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368 AlaglyAlaAlaGlyProAlaGlyAsnProdlyAlaAspGlyGlnProGlyAlaLysGly 387
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231 GlyGluArgGlyProProGlyProGlnGlyAlaArgGlyLeuProGlyThrAlaGlyLeu
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                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                  "Two menus of mouse pro alpha 1(1) collagen gene differ in the size of the 3'-untranslated region.";
Nucleic Acids Res. 16:773-773(1988).
-!- FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen).
-!- SUBGUIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
-!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                             PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains. SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R InterPro; IPRO08164; Cig_helix.
R InterPro; IPRO08166; Cilagen.
R InterPro; IPRO08166; Cilagen.
R InterPro; IPRO0885; Fib_collagen.C.
R InterPro; IPRO01091; WF_C.
R InterPro; IPRO11007; WF_C.
R Ffam; PPO1410; CollFI; 1.
R Ffam; PPO1410; CollFI; 1.
R ProDom; PD002007; Clg_helix; 1.
R ProDom; PD002007; Clg_helix; 1.
R SWART; SW00038; CollFI; 1.
R SWART; SW00214; WKC; 1.
R RROSITE; PS01208; WWC_2; 1.
R PROSITE; PS01208; WWC_2; 1.
R PROSITE; PS01208; WWC_2; 1.
R PROSITE; PS01208; WWC_2; 1.
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TRIPLE-HELICAL REGION.
NONBELICAL REGION.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
A -> V (IN REF. 5).
WW; 3B802E535DF81808 CRC64;
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COLLAGEN ALPHA 1(I) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE.
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Matches:
Conservative:
Mismatches:
Indels:
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L; K03033; AAA37332.1; JOINED.
L; K03034; AAA3732.1; JOINED.
L; K03034; AAA3732.1; JOINED.
L; K03035; AAA3732.1; JOINED.
SS7243; S21626.
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1181 TRIP
1207 NONH
1207 NOLH
56 N-LI
736 CELL
1084 CELL
1450 A ->
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CAA29927.1; -.
AAA37332.1; -.
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MGD; MGI:88467; Collal
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SEQUENCE OF 1-181 FROM N.A.

Chu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,

Myers J., Williams C., Ramirez F.;

Hyman pro alpha 1(1) collagen gene structure reveals evolutionary

conservation of a pattern of introns and exons.";

Nature 310:337-340(1984).
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MEDLINE=84080385; PubMed=6689127;
Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry B.F.,
Prockop D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINES-89025644; PubMed=3178743;

MEDLINES-89025644; PubMed=3178743;

Jacomp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,

Jacomp G., Kuivaniemi H., Etacey A., Shikata H., Baldwin C.T.,

Jacomp G., Kuivaniemi H., Etacey A., Shikata H., Baldwin C.T.,

Structure of a full-length cDNA clone for the prepro alpha 1(I)

Electric of human type I procollagen.";

Biochem. J. 253:919-922(1988)
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01-MAR-1989 (Rel. 10, Last sequence update)
01-OCT-2003 (Rel. 42, Last annotation update)
Collagen alpha 1(I) chain precursor.
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TISSUE=Bone;
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P02452; Q14037; Q15176;
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TISSUE=Skin;
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SEQUENCE OF 1-44 FROM N.A.
MEDILINE-88033098; Pubmeda-2822714;
ROSSDLW C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez F.,
Ade Wet W.J.;
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MEDILINE_9725595 PubMed=9101290;
MEDILINE_97255959 PubMed=9101290;
Kuivaniemi H., Tromp G., Prockop D.J.;
"Mutations in fibrillar collagens (types I II, III, and XI), fibril-associated collagen (type IX), and network-forming collagen (type X) cause a spectrum of diseases of bone, cartilage, and blood vessels.";
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-34 FROM N.A.
MEDLINE-85130970; PubMed=2857713;
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"Fine structural analysis of the human pro-alpha 1 (I) collagen gene.
"Fromcter structure, Alul repeats, and polymorphic transcripts.";
J. Biol. Chem. 260:2315-2320(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rare and some common diseases
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MEDDINE-8722295; PubMed=3108247;
Bateman J.F., Chan D., Walkers I.D., Rogers J.G., Cole W.G.;
Bateman J.F., Chan D., Walkers I.D., Rogers J.G., Cole W.G.;
aretman Jerinatal osteogenesis imperfecta due to the substitution of arginine for glycine at residue 391 of the alpha 1(1) chain of type arginine for glycine at residue
                                                                                                                                                                                                                                                               R.E.;
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MEDLINE=31374476; PubMed=1895312;
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MEDLINE=31374476; PubMed=1895312;
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MEDLINE=88033031; PubMed=3667599;
Vogel B.E., Minor R.R., Freund M., Prockop D.J.;
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J. Biol. Chem. 262:7021-7027(1987)
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MEDLINE=97169389; PubMed=9016532;
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          ZXXBBRITTTAXXBRITTTAXXBRITTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTXAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTTAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXBRITTXAXXB
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"A point mutation in a type I procollagen gene converts glycine 748 of the alpha 1 chain to cysteine and destabilizes the triple helix in a lethal variant of osteogenesis imperfecta."; J. Biol. Chem. 262:14737-14744 (1987).
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Wisubstitution of serine for alpha 1(I)-glycine 844 in a severe
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helix of type I procollagen. The effects of glycine substitutions on
thermal stability are either position of amino acid specific.";
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"RNA sequence analysis of a perinatal lethal osteogenesis imperfecta
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                       SEQUENCE FROM N.A.
MEDLINE=94010892; PubMed=8406456;
Labell T.L., Byers P.H.;
"Sequence and characterization of the complete human thrombospondin 2
CDNA: potential regulatory role for the 3' untranslated region.";
Genomics 17:225-229(1993).
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MEDLINE=21588233; PubMed=11590138;
Mischheimer T.M., Hahr A.G., Harms A.C., Annis D.S., Mosher D.F.;
Mischheimer T.M., Hahr A.G., Harms A.C., Annis D.S., Mosher D.F.;
Mischlide connectivity of recombinant C-terminal region of human thrombospondin 2.";
J. Biol. Chem. 276:45882-45887(2001).
-!- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and cell-to-marrix interactions. Can bind to fibrinogen, fibronectin, laminin and type V collagen.
                                                                                                                                                                                                                                                                                                                                                                                           Thrombospondin 2 precursor.

THBS2 OR TSP2.

THBS2 OR A Sepisary Craniata, Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE-Fibroblast,
MEDLINE-92217961, PubMed=1559694,
Liabell T.L., MGGookey Milewicz D.J., Disteche C.M., Byers P.H.;
"Thrombospondin II: partial cDNA sequence, chromosome location, expression of a second member of the thrombospondin gene family
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-:- SIMILARITY: Belongs to the thrombospondin family.
-:- SIMILARITY: Contains I VWFC domain.
-:- SIMILARITY: Contains 3 EGF-like domains.
-:- SIMILARITY: Contains 3 TSP type-1 domains.
-:- SIMILARITY: Contains 7 TSP type-3 domains.
-:- SIMILARITY: Contains 7 TSP type-3 domains.
-:- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
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01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                CAGAGACTTTGTGGCCCTGGAGGCCTATTAAGCACGACAGAGTATCAGTGGAATTGATCCA 1623
                                                              1624 TAAACCTCCCTGTCCACATCTTGCCCAATGGGGAATGGATCTTTCACCAAAGAGCTCACC 1683
                                                                                                                          eGlyAspAlaCysAspAspAspAspAspAspAspGlyValThrAspGluLysAspAsnCy. 756
 683 yTyrAlaGlyAspGlyLeulleCysGlyGluAspSerAspLeuAspGlyTrpProAsnLe 703
                                                                                                                                                                                                                                                                                                                                                                                            756 sGlnLeuLeuPheAsnProArgGlnAlaAspTyrAsp---LysAspGluValGlyAspAr
                                                                                 716 eLysAspAsnCysProHisLeuProAsnSerGlyGlnGluAspPheAspLysAspGlyIl
                                        703 uAsnLeuValCysAlaThrAsnAlaThrTyrHis---------CysIl
                                                                                                                                                                                         GITGGATGCCTACTTATGAGCTTGACCATACAGCTATCGGTAATCAGAAATA 1810
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                       1684 AGCATTTTCCACAGAG---------
                                                                                                                                                                                                                                                                         7.MXY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Collagen alpha 1(I) chain precursor.
                                                                                                                                                                                                                                                       1460 AA
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InterPro; IPR008160; Collagen.
InterPro; IPR002161; Fib_collagen_C.
InterPro; IPR002181; Fib_collagen_C.
InterPro; IPR001007; VWF.C.
Pfam; PF01410; CoLFI; 1.
Pfam; PF014391; Collagen; 18.
ProDom; PD000007; CIG_helix; 2.
ProDom; PD000007; CIG_helix; 2.
SWART; SM00218; Fib_collagen_C; 1.
SWART; SM00214; VWC; 1.
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TRIPLE-HELICAL REGION.
NONHELICAL REGION (C-TERMINAL).
CELL ATTACHMENT SITE (POTENTIAL).
CELL ATTACHMENT SITE (POTENTIAL).
N-LINKED (GLONAC...) (POTENTIAL).
G -> A. (in OI; severe).
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151
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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PRO-RICH.
D -> G (II
Q -> QQ (C
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EMBL; AXO93078; BAC04045.1; -.
EMBL; AB067474; BAB67780.1; -.
EMBL; AL834230; CAD38908.1; -.
EMBL; AL834259; MBD6.
InterPro; IPR001739; Methyl-CpG_bind.
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SMART; SM00391; MBD; 1
DOMAIN 17 61
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1003 AA;
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Best Local Similarity: ,
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Pukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamateu A., Ishii S., Yamamoto J., Isono Y.,
Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
Isogai T.,
"NEDO human cDNA sequencing project.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                               554 GIGGGAIGAIGICACAGGCAGGIGCAGAACACAGGGCCCCGGCIGIICICCCACIGAAAGA
                                                                                                                                                                                                                                                                               GlyGluProGlyProThrGlyLeuProGlyProPro--------
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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|GlyAsnLysGly-----AspThrGlyAlaLysGlyGluProGly
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10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Methyl-CpG binding domain protein 6.
Homo sapiens (Human).
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MEDLINE=21456161; PubMed=11572484;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----CCCAAGCCACAAGGT 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGATGGCCATCTTGGCTCTATCTTCCACATGTACAGCCACAACATCAGCTCCCT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerThrLeuGlnGlyArgArgPro-----ArgAlaGlnAlaProSerAlaSer----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -> G (IN REF. 1; BAB71176).
-> QQ (IN REF. 1; BAC04045).
; 6C8E8693AA6A3BE6 CRC64;
Wambutt R., Heubner D., Mewes H.-W., Weil B., Wiemann S., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. :- SIMILARITY: Contains 1 methyl-binding (MBD) domain.
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us-09-645-078-1.rsp

RA Kawai J., Shinagawa A., Shi RA Arakawa T., Hara A., Fukuni RA Aizawa K., Izawa M., Nishi RA Saito T., Okazaki Y., Gojok	731 gProProGlnLeuLeuSerProLeuLeuGlyAlaSerLeuLeuGl 746 1263 GGACTGTCCCTGAGCAAATCCACTAAGAGGGTTGAGAAGGCTTTGCTGCCACCTGG 1318	g &
RL J. Biol. Chem. 260:3773-377 RN [5] RP SEQUENCE OF 810-1464 FROM N	rthralathrthraspProGlyAlaSerSerLeuGlyLysAlaProSerAsnSerGlyAr.	d d
	1168GAAAGGCCTGTGTGGCGATGCCATGAATTTTGCTTTTTTTT	6
RX MEDLINE-85131189; PubMed=35	.::::	7 A
		è
RT alpha-1 type-III collagen CRL Gene 61:225-230(1987).	969	; A
Wood L., The		è
RP SEQUENCE OF 1-488 FROM N.A. RX MEDLINE=88167858; PubMed=34	1030	Š 8
G 124 -	uProfheSerdlyLeuglyAspleuserProleuLeuPhoProPr 666	a :
	AGACTICCCGAAIGIAIGAAITCGIGGGAIIGGAAITCTIGCCCCA 10	ò
	638GlyGluGlySerAlaGluGlyAlaGlyGlyProSerGlyGl 651	ପ୍ର
	939 ACCIGCTIGIGCGCIAIGAGGACCIGGCICGAGC	ò
RA Villalon D.K., Muzny D.M., RA Fahey J., Helton E., Kettem	618 oSerAsnLeuLeuAlaSerPheLeuProLeuLeuAlaLeuGlyFroThrAlaGlyAsp 637	ą
	. 907GAGGAACGCT 938	ò
	599 1AlaSerLeuLeuProProProPerAspLeuLeuProProProSerAlaProPr 618	qq
RA Diatchenko L., Marusina K.,	861 TGATGCAGGTCATCTGCCAAAGCCAGCTGGAGATCTACAAGACCAT 906	ò
	:: 587	셤
	801 GTCGCATTGTGATGGGGCAGCATGAGAAAACTCAAGAAGGAGGACCAACCCTATG 860	ò
		: <u>a</u>
	をしまり出来ではなり出かれなりです。 まっちゅうしょ まりょうし フェー・ファー・ファー・ファー・ファー・ファー・ファー・ファー・ファー・ファー・ファ	ě
RT "The mouse type-III procoll RT complete DNA sequence.";		셤
	694	à
RC STRAIN=CS78L/6 X DBA, TISSU	 543 uProLeuSerLeuGlyGlnProProProSerProLeuLeuAsnHisSerLeuPheGlyVa 563	q
	690 ACCC	λŏ
OC Mammalia, Entheria, Rodenti	525GlnGlyLeuAlaLeuSerGlyAlaGlyPheProGlyMetLeuGlyAlaLeuProLe 543	qq
	651 TGCTCAAGGAGGTGCGCTT	δ
Collagen alpha 1(III)	506 AlaCysProLeuProProLeu-AlaGlyGlyGlyAlaPheProPheProSerProGlu 524	qq
DI 01-400-1900 (Nel. 90) (Last DI 15-UUL-1999 (Nel. 38) Last DH 15-MAD-2004 (Del 43 1994	591 TGTGCAGTCAACAGCCCTTTGAGGTGGTGGAGAAGGCCTGCCGCTCCTACAGCCACGTGG 650	ζ
CAIS MOUSE PO8121; Q61429;		qq
CA13 MOUSE	□ <	ò
o yearbearease.		qq
	489 CCAGCCTCTTTCAGTGGGAGAACAGCCGGGCCCTGTGTTCTGCACCTGCCT 539	à
Db 746 YASpLeuserserLeutn		qa
746		

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746 yAspleuSerSerleuThrSerSerProdlyAlaLeuProSerleuLeuGlnProProdl 765 | 1319 TOTAACCTAGT 1331 | FORTAACCTAGT 1331 | FORTAACCTAG
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Kadota K., Mateuda H.A., Ashburner M., Batalov S., Casavant T., A Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubii F., Suzuki R., Tomita M., Wagner L., Washio T., A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Edidor T., Furuno M., Aono H., Baldarelli R., Barsh G., A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., A Saski H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wiming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., A., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                 Metsaeranta M., Toman D., de Crombrugghe B., Vuorio E.,
"Specific hybridization probes for mouse type I, II, III and IX
"Specific hybridization probes for mouse type I, II, III and IX
Blochim. Blophys. Acta 1089:241-243(1991).
-!- FUNCTION: Collagen type III occurs in most soft connective tissues
along with type I collagen.
-!- SUBUNIT: Trimers of identical alpha I(III) chains. The chains are
linked to each other by interchain disulfide bonds. Trimers are
also cross-linked via hydroxylysines.
-!- PTM: Proline residues at the third position of the tripeptide
repeating unit (G-X-Y) are hydroxylated in some or all of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIM: O-linked glycan consists of a Glc-Gal disaccharide bound to the oxygen atom of a post-translationally added hydroxyl group (By
                                                                                                                                                                                                                                                                       'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01208; VWFC 1; 1.
PROSITE; PSS0184; VWFC 2; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
SIMILARITY: Contains 1 VWFC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A27353; A27353.

PIR; S5885; S5985.

MGD; MGD; B8453; Collad.

INCEMPC; IPRO08160; Collagen.

INCEMPC; IPRO08160; Collagen.

INCEMPC; IPRO1816; Fib_collagen.

INCEMPC; IPRO1816; Fib_collagen.

INCEMPC; IPRO1919; WWF.C.

Pfam; PF01410; Collagen; 18.

ProDom; PD000079; Collagen; 18.

ProDom; PD000079; Fib_collagen.C; I.

SMART; SM00214; WWC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M18933; AAA37338.1; --
KK03037; -; NOT ANNOTATED_CDS.
AK01944; BAB31724.1; --
K57983; CAA41048.1; --
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91274355; PubMed=2054384;
                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1442-1464 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC043089; AAH43089.1; -. BC058724; AAH58724.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X52046; CAA36279.1; -.
                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001).
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SIGNAL
PROPEP 2
CHAIN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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-----Asn-GlyGluArgGlyProProdlyProGlnGlyLeuProGlyGln---- 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .064 TGCCTCGGGTGATGTTATGCACCCAGGTCTGAAGATGGGGCCAAGAATTCCAATCCCACGA 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                               829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              341 GlyserProGlyProLeuGlyIleAlaGlyLeuThrGlyAlaArgGlyLeuAlaGly--- 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||||||||:::
921 ProlysGlyAspAlaGlyGlnProGlyGluLysGlyProProGlyAlaGlnGlyProPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              671 AGAAGOGCACCTCCTTGAGCACCACGTGGCTGTAGGAGCGGCAGGCCTTCTCCCACCACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||
|------GlylleLysGlyGluSerGlyLysProGlyAlaSerGlyHis-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1124 CCTGGGAGACATTAAGGGCATCCCTGGCATTTGTGTGGAAAGCGTGGTCACCCATGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     842 GlyProThr---GlySerSerGlyProAlaGly---ProProGlyProGlnGlyValLyS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1004 ATTCATACATTCGGGAAGTCTGGGCCACAGGGGCTCGAGCCAGGTCCTCAT-----AGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             950 GCACAAGCAGGTAĞCGTTCCTGCAGGGCCTTGGGCAAGGACTGGATGGTCTTGTAGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           890 CCAGCTGCCTTT-----GGCAGA------TGACCTGCATCACATAGTAGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                               814 proglyGlnAsn---GlyGluPro---GlyAlaLysGlyGluArgGlyAlaPro----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||||||
|GlyProProGly------ProSerGlyAlaProGlyLy8------
                           NONHELICAL REGION (N-TERMINAL).
TRIPLE-HELICAL REGION
O-LINKED (GAL. .) (BY SIMILARI)
HYDROXIATION (BY SIMILARIY).
HYDROXIATION (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
CARBOXYL-TERMINAL PROPEPTIDE
                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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139.50
32.878
28.378
3.778
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11195
1464
262
262
283
889
976
1105
11195
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1093 109
1105 110
1195 119
1196 AA;
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                                                                                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                             MOD_RES
MOD_RES
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.

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STRAIN=C57BL/6J; TISSUE=Mammary gland;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.R., Blat N.R.,

Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.R., Haich F.,

Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.R., Haich F.,

Appleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheefer T. E.,

Brownstein M.J., Usdin T.B., Ponaldo M.F., Carninci P., Mullaly S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Glubs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Willalon D.K., Munny D.M., Scheergren E.J., Lu X., Gibbs R.A.,

Nilalon D.K., Manny D.M., Scheergren E.J., Lockson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakesley R.W., Tucchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Nirzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Rohnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

R. Human and mouse coph, sequences ", Marra M.A.;

R. Human and mouse coph, sequences ", Marra M.A.;

R. Human and mouse coph, sequences ", Marra M.A.;

R. Human and mouse coph, sequences ", Marra M.A.;

R. Human and mouse coph, sequences ", Marra M.A.;

R. Human and mouse coph, sequences ", M. Schein E.D., Dickson M.C.)
                                                                                                                                                                                                                          1033 gGlyGluAsnGlySerProGly--AlaProGlyAlaProGlyHisProGlyProProGly 1052
                           1018 pGlyGlnPro-------GlyArgAspGlySerProGlyGlyLysGlyAspAr 1033
                                                                                                                                                                                  371 AGGTCATCCACCACGTGCCAGGCGGGCTCCATCAGGTAGAAACATCTGGGTGCTGCCCAA 312
                                                                                                                                                                                                                                                                              311 AAAGCTGCCCCACAAAAGAAGAGCCAGGAGCGCCAGGAAGACAGAACCAGCACGTGCATGC 252
                                                                                                                                                                                                                                                                                                                                                                           251 GCTCGGGCTGTGCCTTCATAGACAGGGAGCTGATGTTGTGGCTGTACATGTGGAAGAATA 192
491 TGGACTGTCTCCGGGGGACCAGGTTCCATGTAGGCATCAAAGACGCTCATGTCGCACAAGA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

TISSUB=Calvaria;

MEDLINE=9237043; PubMed=1505972;

MEDLINE=9237043; PubMed=1505972;

"Sequence analysis of a full-length cDNA for the murine pro alpha 2(1) collagen chain; comparison of the derived primary structure with denomic 13:1345-1346(1992).
                                                                                                                                                                                                                                                                                                          431 AGACGGCCCGTATCAGATCCCGCACACCATGTGCAGCATCCAGGCGGTGCTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1070 ------GlyProSerGlyAlaProGlyProAlaGlyAla 1080
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Collagen alpha 2(I) chain precursor.
COLLA2 OR COLA2.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ā
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                         MEDLINE=92084969; PubMed=1748823;
Phillips C.L., Lever L.W., Pinnell S.R., Quarles L.D.,
Wenstrup R.J.;
"Construction of a full-length murine pro alpha 2(1) collagen cDNA by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hydroxyapatite. Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
                                                                                                                                                                                                                              MEDLINE-87289560; PubMed=3033494;

MEDLINE-87289560; PubMed=3033494;

Rossi P., de Crombrugghe B.; Specific transcriptional enhancer in the first incron of a call-specific transcriptional enhancer in the first incron of the mouse alpha 2 (type I) collagen gene.";

Proc. Natl. Acad. Sci. U.S.A. 44:5590-5594(1987).

- I FUNCTION: Type I collagen is a member of group I collagen (fibrillar forming collagen).

- I SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.

- I TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
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CONVERED TO AN ALDEHYDE GROUP THAT
INVOLVED IN CROSS-LINKING
(BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
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Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Signal; Pyrrolidone carboxylic acid. SIGNAL 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY).
COLLAGEN ALPHA 2(1) CHAIN.
CARBOXYL-TERMINAL PROPEPTIDE
(BY SIMILARITY).
PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
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V -> A (IN REF. 4).
R -> TT (IN REF. 1).
MW; 0D17DF5D6C1452D1 CRC64;
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PIR, AA3291, AA43291.
MGI 88468; Collad.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Collagen.
InterPro; IPR00885; Fib_collagen_Cream, PF01410; Colf. 1.
Pfam; PF01391; Collagen; 18.
ProDom; PD00007; Clg helix; 6.
ProDom; PD002078; Fib_collagen_C; 1.
                                                                                                                                               the polymerase chain reaction.";
J. Invest. Dermatol. 97:980-984(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X58251; CAA41205.1; -.
EMBL; BC007158; AAH07158.1; -.
EMBL; BC042503; AAH42503.2; -.
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US-09-645-078-1 (1-2043) x CA21_MOUSE (1-1372)

1372 104 115 1134 24

> Matches: Conservative: Mismatches: Indels:

0.0279 138.50 30.67% 26.80% 3.74%

> Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores:

Gaps:

::: Db 781 yserArgG] Qy 96 CTTCCTGG Db 793 yPheProG1 RESULT 10 CA12 HIMAN	ID CA12 HUMAN STI AC P02458; DT 21-JUL-1966 (Rel. DT 01-JAN-1990 (Rel. DT 15-MAR-2004 (Rel. DB COllagen alpha 1(RT "Promoter region." RL Gene 44:11-16(198 RN [3] RP SEQUENCE OF 422-1 RA SEMILES F.;		SEQU SEQU Elim Vuor Coor		RN 1/1 LN 127- RX MEDLINE-86104139; RA Nunez A.M., Franc RT "Isolation and pa RT a human pro-alpha RT restriction fragm RL Blochemistry 24:6 RN [8]	RP SEQUENCE OF 1176- RX MEDLINE=84118798; RA Strom C.M., Uphol RT "Isolation and c? RT the human type II
		-GCATCACATAGGGTTGGTCCTCCTTCT 837 :::			GGGATGATTTCATCTTGTGGGATGA 546 Y 637 TTCTCCCACTGAAGAGGCTGGACT 486	TCTCCGGGGACCAGGTTCCATGTAGGCATCAAAGACGCTCATGT 441	CCACACGTGCCAGGCGGCT 345	GCTGCCCRAMAMAGTGCCCCACRAMAMAGAGCCAGAGGAA 274	CATCTGGGAAACCAGAAACAGCAGG 154 ::
1127 AAGCCTGGGACACATTAAGGCCATCCCTGGCATTTGTGTGGGAAAGCGTGGTCACCCTGTGC		887 GCTGGCTTTGGCAGATGACCTGCATCACATAGTAGGGTTGGTCCTCCTTCT	TGCGTTCTCGGGAACGGAACACGGACACGG GlyGluPheGlyLev TGAGGAGGGTCTTTCAGCAGGG		605 GCTGTTGACTGCACAGGGGGGGGGGGGGGGATTTCATCTTGTGGGTGATTG 628 GlyGluAlaGlyAlaValGlyAlaProGly	485 GGACGCTCCGGGGACCAGGTTCCATGTAGGCATCAAAGACGCTCATGT	380 TCTGCTTGAAGGTCAT	320GCTGCCCAAAAAGCTGCCCCAAAAAGAAGAAGAAGGGCCAGGAAAAGAAGAAGGCCAGGAAAAGAAG	213 TGGCTGTACATGTGGAAGAATAGAGCCAAGATGGCCATCTGGGAAACCAGAAACAGCAGG [
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7-1289 FROM N.A.
9; PubMed=3002437;
ncomano C., Young M.F., Martin G.R., Yamada Y.;
partial characterization of genomic clones coding for ha I (II) collagen chain and demonstration of genent length polymorphism at the 3' end of the gene."; 6343-6348(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.
;; PubMed=2587267;
Ramirez F., Machado M., Horton W.;
tence of the full length cDNA encoding for human type
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PubMed=387598;
c)cer N.G.=3875598;
c)cer M.G.=3875599;
and characterization of the human type II collagen
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8; PubMed=6320112;

characterization of genomic clones corresponding to

II procollagen gene.";
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1; PubMed≈2825137;
o T., Vuorio E.;
of the single polyadenylation site of the human pro
lagen gene.";
es. 15:9499-9504(1987).
                                                                                                                                                                                                                                                                                                                                                                         man).
oa; Chordata; Craniata; Vertebrata; Euteleostomi;
ia; Primates; Catarrhini; Hominidae; Homo.
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. 13, Last sequence update)
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(II) chain precursor [Contains: Chondrocalcin].
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4; PubMed=3021582;
10 K., Martin G.R., Yamada Y.;
1 of the human pro-alpha 1(II)-collagen gene.";
186).
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.; PubMed=3840017;
.ae J.K., Vuorio T., Kauppinen S., Knowles J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          988) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                               PRT; 1418 AA.
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s. 17:9473-9473(1989).
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:183-188(1985).
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US-09-645-078-1 (1-2043) x CA12 HUMAN (1-1418)
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RARENE RELEVANTE RELEVANTE
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Kuivaniemi H., Tromp G., Prockop D.J.;
"Mutations in collagen genes: causes of rare and some common diseases
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97255959; PubMed=9101290; Kuivaniemi H., Tromp G., Prockop D.J.; Mutations in fibrillar collagens (types I, II, III, and XI), fibrilassociated collagen (type IX), and network-forming collagen (type X) cause a spectrum of diseases of bone, cartilage, and blood vessels.";
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Eyre D.R., Weis M.A., Moskowitz R.W.; 
"Cartilage expression of a type II collagen mutation in an inherited 
form of osteoarthritis associated with a mild chondrodysplasia."; 
J. Clin. Invest. 87:357-361(1991).
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MEDIINE-91291116; PubMed=2064612;
Bateman J.F., Hannagan M., Chan D., Cole W.G.;
Characterization of a Type I collagen alpha 2(I) glycine-586 to valine substitution in osteogenesis imperfecta type IV. Detection of the mutation and prenatal diagnosis by a chemical cleavage method.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=90370826; PubMed=1975693; Ala-Kokko L., Baldwin C.T., Moskowitz R.W., Prockop D.J.; "Single base mitation in the type II procollagen gene (COL2A1) as cause of primary osteoarthritis associated with a mild chodurodysplasia."; Proc. Natl. Acad. Sci. U.S.A. 87:6565-6568(1990).
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Cohn D.H., Eyre D.R.;
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Hollister D.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89266907; PubMed-2543071;
Lee B., Vissing H., Ramirez F., Rogers D., Rimoin D.;
"Identification of the molecular defect in a family wi
spondyloepiphyseal dysplasia.";
Science 244:978-980(1989).
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MEDLINE=9003699; PubMed=2572591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93054548; PubMed=1429602;
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MEDINE=39140139; PubMed=8423604;
MEDINE=39140139; PubMed=8423604;
COLE W.G., Hall R.K., Rogers J.G.;
"The clinical features of spondyloepiphyseal dysplasia congenita resulting from the substitution of glycine 997 by serine in the alpha 1(II) chain of type II chape 11 (II) chain of type II 35(1993).
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MEDLINE=92262484; PubMed=1374906;

Horton W.A., Machado M.A., Ellard J., Campbell D., Bartley J.,

Ramirez F., Vitale E., Lee B.;

"Characterization of a type II collagen gene (COL2A1) mutation

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Proc. Natl. Acad. Sci. U.S.A. 89:4583-4587(1992).
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II gene
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PFB-1994 (Rel. 28, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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"Chemical studies on the cyanogen bromide peptides of collagen. Amino acid sequence of alpha 1-CB4.";
Biochemistry 10:2076-2081(1971).
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MEDLINE=67165368; PubMed=4290711;
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MEDLINE=70085124; PubMed=5411206;
SEQUENCE OF 1-19.
MEDLINE=69155173; PubMed=5777344;
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                                                                                                                                                                       ochemistry 8:63-71(1969)
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330 SerArgGlyPheProdlyAlaAspGlyValAlaGlyPro-----LysGlyProAlaGly 347
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                   PTM: O-linked glycan consists of a Glc-Gal disaccharide bound to the oxygen atom of a post-translationally added hydroxyl group.
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9DC3114204AC4918 CRC64;
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InterPro; IPR008160; Collagen.
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PRODOM; PD000007; Clg helix; 1.
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ProDom; PD0002078; Fib_collagen_C; 1.
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SMART; SM00214; VWC; 1.
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MEDLINE=72243016; PubMed=5047697;

Eyre D.R., Glimcher M.J.;

"Evidence for a previously undetected sequence at the carboxyterminus of the alpha 1 chain of chicken bone collagen.";

Biochem. Biophys. Res. Commun. 48:720-726(1972).
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 981-1453 FROM N.A. MEDIALIZE-81160715, PubMed=6927845; PELIAE-81160715, PubMed=6927845; Pullar F., Boeddker H.; Soeddker H.; Sequence determination and analysis of the 3' region of chicken proalpha 1(1) and pro-alpha 2(1) collagen messenger ribonucleic acids including the carboxy-terminal propeptide sequences."; elichemistry 20:996-1006 (1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=82231995; PubMed=7093229; Higherger U.H., Corbett C., Dixit S.N., Yu W., Seyer J.M., Higherger U.H., Corbett C., Dixit S.N., Yu W., Seyer J.M., Manda A.H., Grobett C., Dixit S.N., Yu W., Seyer J.M., Corpett G. J., Grobett G. Chick skin collagen alpha 1(1)-CB8 and the complete primary structure of the helical portion of the chick skin eiloghemistry 21:2048-2055 (1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (fibrillar forming coliagen).
SUBUNIT: Trimers of one alpha 2(I) and two alpha 1(I) chains.
TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-144 FROM N.A.
MEDLINE=88007542; PubMed=2820966;
Finer M.H., Aho S., Gerstenfeld L.C., Boedtker H., Doty P.;
Finer M.H., sequences located within the promoter region and the
first intron of the chicken pro-alpha 1(1) collagen gene.";
J. Biol. Chem. 262:13323-13332(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hydroxyapatite. PTM: Proline residues at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Showalter A.M., Pesciotta D.M., Eikenberry E.F., Yamamoto T., Pastan I., Decrombrugghe B., Fietzek P.P., Olsen B.R.; "Nucleotide sequence of a collagen cDNA-fragment coding for the carboxyl end of pro alpha 1(I)-chains."; FEBS Lett. 111:61-65(1980).
-!-FUNCTION: Type I collagen is a member of group I collagen
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-153 FROM N.A.
MEDLINE=88056316; PubMed=3678834;
Finer M.H., Boedtker H., Doty P.;
"Construction and characterization of cDNA clones encoding the of the chicken pro alpha 1(I) collagen mRNA.";
Gene 56:71-78(1987).
                                                                                                                                                                                    21-JUL-1986 (Rel. 01, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-2003 (Rel. 42, Last annotation update)
collagen alpha 1(1) chain precursor.
                                                                                                                                                PRT; 1453 AA
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                                                                                                                                                STANDARD;
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                      38 000 36
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS50184; VWFC 2; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
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HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
HYDROXYLATION.
F -> L (IN REF. 5).
Q -> H (IN REF. 6).
Q -> H (IN REF. 6).
chains. Pro-1153 is the only 3-hydroxypro and the only hydroxylated proline in position X. SIMILARITY: Contains 1 VWPC domain.
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COLLAGEN ALPHA 1(1) CHAIN.
C-TERMINAL PROPEPTIDE.
VWFC.
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Matches:
Conservative:
Mismatches:
Indels:
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480 GlySerArgGlyPheProGlyAla 487

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172 ProhladlyProbragglyLeuProglyProproglyAlabrodlyProglnglyPhedIn 191 944	779TTGTGCGTTCTCGGGAACGGACCCGGGGGTCCCGGACCAGGTGCACGA 726 258 GlyPheSerGlyLeuAspGlyAlaLysGlyGlnProdlyProAlaGlyProLysGlyGlu 277 725 TATGCAGGTTGAGGGGTCTTTCAGCAGGGGTAGAGGGACTGCA 678 [1] 278 ProGlySerProGlyGluAsnGlyAlaProGlyGlnMetGlyProArgGlyLeuPro 296 677 GGTTGAAGAAGACGCACTCCTTGAGCACCAGTGGTGTAAGAGGCAGGCAGGCTTC 621 [278 ProGlySerProGlyGluAsnGlyAlaProGlyGlnMetGlyProArgGlyLeuPro 296 677 GGTTGAAGAAGACGCACTCCTTGAGCACCAGTGGCTGTAAGAGGCGCAGGCATCT 621 [278 ProGlySerProGlyProSerGlyProAlaGlyAnaArgGlyAsnAspGlyAla 316 620 CCACCACCTCAAAGAGCTGTGACTGCAAAGAGCCTGCAGTGAGTG	GAAAGAGGCTGCACTCCGGGGACCAGGTTCCATGTAGGCATCAAGA [413 SerglyÄlaProGlyProLysGlyAsnSerGlyGluProGlyÄläProGlyAsnijyGly 432 287 CAGAGCGCCAGGAACACACACACACACAGCATCCCTCGCCTTCATAGACA 228 33 ASpThrGlyAlaLysGlyGluProGlyProAlaGlyValGlnGlyProProGlyProAla 452 227 GGGAGCTGATGTTGGCTGTACATGTGGAAGAATAGAGCCAAGATGCCATCTGGGAA 168 453 GlyGluGluGlyLySArgGlyAlaArgGlyGluProGlyProAlaGlyLeu 469 167 CCAGAAACAGCAGGAGCTTCATTTTTTAGGCAGTAGCATTGTGCTGAAGTGGAAGACCT 108 167 CCAGAAACAGCAGGAGCTTCATTTTTTAGGCAGTAGCATTGTGCTGAAGTGGAAGACCT 108 167 CCAGAAACAGCAGGAGCTTCATTTTTTAGGCAGTAGCATTGTGCTGAAGTGGAAGACCT 108 168 CAGAAACAGCAGGAGCTTCCTTTTTTTAGGCAGTAGCATTGTGCTGAAGTGAAGACCT 108 109 TGTGGCTTGGGCTTCCTTTTTTTTAGGCAGTAGCATTGTGCTGAAGTAGAATAGTAAATAGTAAATAGTAAATAGTAGTAG
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RESULT 13

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200 GlnProvalThrSerAspCysHisProLeuCysAlaTrpThrLysTrpPheAspValAsp 219
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                              ThrThrSerThrThrSerGlyProGlyThrThrProSerPro------ValPro
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             CCGTCTTCTTGTGCGACATGAGCGTCTTTGATGCCTACATGGAACCTG-----GTCCCC
                                                                    GGAGACAGTCCAGCCTCTTTCAGTGGGAGAACAGCCGGGCCCTGTGTTCTGCACCTGCCT
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CSHLSGPAPGLAELLWPCIQPAVLGT (IN REF. 4)
WW; 37CEASFPADC8A28DE CRC64;
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CRSPVSPTPARAPPTSSTLAS (IN REF. 2).
L -> P (IN REF. 3).
C -> S (IN REF. 2).
GDTQHSEAEPEPSQEAESGSWERGVPVSFMH --
RRRRNPSPARRQRVGAGREASSVPHALTS (IN
      constituent;
GO, GO:0005201; F:extracellular matrix structural conigo; GO:000155; P:cell adhesion; NAS.
InterPro; IPR006208; Oys.knot.
InterPro; IPR006209; Oys.knot.
InterPro; IPR00219; TIL_Cysrīch.
InterPro; IPR001007; VWF_C.
IPEMP: PF00007; Cys.knot; 1.
PROSITE; PS00125; CTCK_1; 1.
PROSITE; PS01225; CTCK_2; 1.
PROSITE; PS01208; VWFC_1; 2.
PROSITE; PS01208; VWFC_1; 2.
PROSITE; PS01208; VWFC_2; 2.
REPEMT; Glycoprotein.
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1070 1022 AGAAAGCCTGTGGCCATGCATGAATTTGCTGGGCTACCGCCACGTCAGATCTGAACAAG 1226 1227 AACAGAGAAAÇÇTGTTGCTGGATCTTCTGTCTACCTGGACTGTCCCTGAGCAATCCACT 1286 AAGAGGGTTGAGAAGGCTTTGCTGCCACCTGGTGTCAGCCTCAGTCACTTTCTCTGAATG 1346 TGGGTG---ACCACGCTTTCCACACAAATGCCAGGGATGCCCTTAATGTCTCCCAGGCTT 1127 239 257 GluSerHisProGluValAsnIleGluHisLeuGlyGlnValValGlnCysSerArgGlu 277 339 GluGlyLeuValCysArgAsnGlnAspGlnGlnGlnGlyProPheLysMetCysLeuAsnTyr :::||| 220 PheProSerProGlyProHisGlyGlyAspLysGluThrTyrAsnAsnIlelleArgSer ------TGCCCCATCTTCAGACCTGGGTGCATAACATCACCCGAGGCAAGGGCA 240 GlyGluLysIleCysArg-----ArgProGluGluIleThrArgLeuGlnCysArgAla TGGCCCAGACTT----CCCGAATGTATGAATTCGTGGGATTGGAATTCT-----1287

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Length:
Matches:
Conservative:
Mismatches:
Indels:

0.032 137.50 32.76% 23.56% 3.67%

Percent Similarity: Best Local Similarity: Query Match:

Alignment Scores:

Gaps:

US-09-645-078-1 (1-2043) x MU5A_HUMAN (1-1233)

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                                                                      1407 IGTGAGTIGTGTCCACACGTGCTCAAGCAGAAGACTTTTGTGTCCATGCTTGTGTCTAG
                                                                                                        1467 AAAACAGACTGGGGAACCTTATGTGAGCAGCACATCCCACCAGTGAAACA------
                                                                                                                                                                                 364 ------AsnValAlaAspArgLeuTyrFroAlaGlySerThrIleTyrArgH
                                                                                                                                                                                                                                            379 isArgAspLeuAlaGlyHisCysTyrTyrAlaLeuCysSer------
                                                                                                                                                                                                                                                                                                                                                                      1623 ATAAACCTCCCTGTCCACATCTTGCCCAATGGGGAATGGATCTTTCACCAAAGAGCTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                               1683 CAGCATTTTCCACAGAGATGCGAATTCTGAGCCCTTGGAGTTCCCAATGGGATTCAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE=89123368; PubMed=2914927; Woodbury D., Benson-Chanda V., Ramirez F.; Moodbury D., Benson-Chanda V., Ramirez F.; Amino-terminal propeptide of human pro-alpha 2(V) collagen conforms to the structural criteria of a fibrillar procollagen molecule."; J. Biol. Chem. 264:2735-2738(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1227-1496 FROM N.A.
MEDLINE=85289337; PubMed=2411731;
Myers J.C., Loidl H.R., Seyer J.M., Dion A.S.;
"Complete primary structure of the human alpha 2 type V procollagen COOH-terminal propepties", J. Biol. Chem. 260:11216-11222(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genetic distance of two fibrillar collagen loci, COL3A1 and COL5A2 located on the long arm of human chromosome 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 398-1496 FROM N.A.

MEDLINE=87146331; PubMed=3029669;

MEDLINE=87146331; PubMed=3029669;

MEDLINE=87146331; PubMed=3029669;

"The pro alpha 2(V) collagen gene is evolutionarily related to the major fibrillar-forming collagens.";

Nucleic Acids Res. 15:181-198(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1449-1496 FROM N.A.
MEDLINE-89138450; PubMed=3224983;
Tsipouras P., Schwartz R.C., Liddell A.C., Salkeld C.S., Weil D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1988 (Rel. 07, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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1. Med. Genet. 35:846-848(1998).

1. 1. EUNCTION: Type V collagen is a member of group I collagen

(fibrillar forming collagen). It is a minor connective tissue

(component of nearly ubiquitous distribution. Type V collagen binds

to DNA, heparan sulfate, thrombospondin, heparin, and insulin.

1. SUBDNIT: Trimers of two alpha 1(V) and one alpha 2(V) chains in

most tissues and trimers of one alpha 1(V), one alpha 2(V), and

one alpha 3(V) chains in placenta.

1. PTM: Prollines at the third position of the tripeptide repeating

one alpha 3(V) chains in placenta.

1. PTM: Prollines at the third position of the tripeptide repeating

unit (G-X-Y) are hydroxylated in some or all of the chains.

1. DISEASE: Defects in COLSA2 are a cause of Bhlers-Danlos syndrome

type I (EDS-I) [MIN: 130000]; also known as Ehlers-Danlos syndrome

gravis. EDS-I is an autosomal dominant.

1. DISEASE: Defects in COLSA2 are a cause of Ehlers-Danlos syndrome

type II (EDS-II) [MIN: 130010]; also known as Ehlers-Danlos

syndrome mitis. Inheritance is autosomal dominant.

2. SIMILARITY: Contains I VMPC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burrows N.P.; "A single base mutation in COLSA2 causes Ehlers-Danlos syndrome type II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              Michalickova K., Susic M., Willing M.C., Wenstrup R.J., Cole W.G., "Mutations of the alpha2(V) chain of type V collagen impair matrix assembly and produce Ehlers-Danlos syndrome type I."; Hum. Mol. Genet. 7:249-255(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.B., Pope F.M.,
                                                                                                                                                                                                                         MEDLINE-94237164; PubMed-8181482; Moradi-Ameli M., Rousseau J.C., Kleman J.P., Champliaud M.F., Moradi-Ameli M., Rousseau J.C., Kleman J.P., van der Rest M.; Boutillon M.M., Bernillon J., Wallach J.M., van der Rest M.; Diversity in the processing events at the N-terminus of type-V collagen.";
                                                                                                                            "Isolation of the alpha 3-chain of human type V collagen and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005588; C:collagen type V; TAS.
GO; GO:0008151; P:cell growth and/or maintenance; TAS.
InterPro; IPR008161; Clg_helix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98455031; PubMed=9783710;
Richards A.J., Martin S., Nicholls A.C., Harrison
                                                                                                                                              characterization by partial sequencing.'
Biol. Chem. Hoppe-Seyler 373:69-75(1992)
                                                                                                                                                                                                                                                                                                                                                            Eur. J. Biochem. 221:987-995(1994).
                                                                                   MEDLINE=92239022; PubMed=1571108;
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EMBL; X0478; CAA28464.1; --
EMBL; M11718; AAA52558.1; --
PIR; A31427; CGHUZV.
PDB; JA9A; 18-NOV-98.
Genew; HGNC:2210; COL5A2.
MIM; 120190; --
Genomics 3:275-277(1988)
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                                           OF 208-227
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                                                                                                  --GluAspGlyArgProGlyPro
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Campbell B.G., Wootton J.A.M., McLeod J.N., Minor R.R.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Type I collagen is a member of group I collagen
(fibrillar forming collagen).
-!- SUBUNITY: Trimers of one alpha 2(I) and two alpha 1(I) chains.
-!- TISSUE SPECIFICITY: Forms the fibrils of tendon, ligaments and bones. In bones the fibrils are mineralized with calcium
LysglySerGlnGlyAgpProGlyArgProGlyGluProGlyLeuProGlyAla----
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR00885; Fib_collagen_C.
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Pfam; PF01391; Collagen; 17.
ProDom; PD000007; Clg_helix;
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PROSITE; PS01208; VWFC_1; 1.
PROSITE; PS01204; VWFC_2; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Glycoprotein; Collagen; Signal; Ehlers-Danlos syndrome; Disease mutation; 3D_structure.
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-> F (IN REF. 6).

-> T (IN REF. 3).

-> S (IN REF. 3).

-> Q (IN REF. 4).

-> A (IN REF. 4).

82827C17A8644F5A CRC64;
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CARBOXYL-TERMINAL PROPEPTIDE
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Matches:
Conservative:
Mismatches:
Indels:
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         InterPro; IPR0008160; Collagen.
InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001811; Fibrinogen_C.
InterPro; IPR001007; VWF_C.
Pfam; PF01341; Collagen; 18.
Pfam; PF01341; Collagen; 18.
Pfam; PF000007; Cig_helix; 5.
ProDom; PD000007; Cig_helix; 5.
SMART; SM00214; VWC; 1.
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CTGAAAGAGGCTGGACTGTCTCCGGGGACCAGGTTCCATGTAGGCATCAAAGACGCTCAT 443
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         ysGlyGluGlnGlyProAlaGlyProProGlyPheGlnGlyLeuProGlyProAlaGlyT 563
                                                                                                                                                                                                                                                                                                                      643 lydluArgdly-----AlaAlaGly-----IleProGlyGlyLysGlyGluLysGlyG
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386 luAlaGlySerAladlyProSerGlyProProGlybeuArgGlySerProGlySerArgG 406
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| GlyGluSerGlyAsnLysGlyGluProGly--SerAlaGlyAlaGlnGlyProPro---
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                                                                                                                                                                                          SIMILARITY, CONVERTED TO AN ALDEHYDE GROUP THAT IS INVOLVED IN CROSS-LINKING (BY
ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM00038; COLFI; 1.
Extracellular matrix; Connective tissue; Repeat; Hydroxylation; Collagen; Signal; Pyrrolidone carboxylic acid.
SIGNAL 1
                                                                                                                       COLLAGEN ALPHA 2 (I) CHAIN, CARBOXYL-TERMINAL PROPEPTIDE (BY SIMILARITY).
                                                                                                                                                 PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
                                                                                           (BY
                                                                                                                                                                                                                                 SIMILARITY).
W; CD9369595080BCD4 CRC64;
                                                                         POTENTIÁL.
AMINO-TERMINAL PROPEPTIDE
SIMILARITY).
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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O55000 rattus norv
O86xj2 homo sapien
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SEQUENCE FROM N.A.
TISSUE=70nsil;
MEDLINE=99264316; PubMed=10330415;
Bistrup A., Bhakta S., Lee J.K., Belov Y.Y., Gunn M.D., Zuo F.R.,
Huang C.C., Kannagi R., Rosen S.D., Hemmerich S.;
Huang C.C., Kannagi R., Rosen S.D., Hemmerich S.;
Shifotransferases of two specificities function in the reconstitution of high endothelial cell ligands for L-selectin.";
J. Cell Biol. 145:899-910(1599).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GST3...
Homo sapiens (Human).
Elbaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 24, Last annotation update)
N-acetylglucosamine 6-O-sulfotransferase (L-selectin ligand sulfotransferase GST-3).
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Q9Y4C5
Q9EQC0
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Q9Y5R3
  Command line parameters:
-MODEL=frame+ LTB, model - DEV=xlp
-MODEL=frame+ LTB, model - DEV=xlp
-MODEL=frame+ LTB, model - DEV=xlp
- Gord 1/USFTO spool p/US09645078/runat 06052004 104559 21739/app query.fasta_1.2183
- DE=SPTREMEL_25 - TORMT-fastan - SUFFIX=rspt - MINNATCH=0.1 - TOOPCL=0 - TOOPEXT=0
- UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
- UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
- OOGALIGN=200 - TRR_SCORE=pct - THR_NAX=100 - TRR_RIN=0 - AALIGN=15 - MODE=LOCAL
- OOTENT=pct - NORM=ext - HEAPSIZE=500 - MINNEND - MAXIZN=200000000
- USER=US09645078 @CGN 1 1 112 @runat 06052004 104559 21739 - NCPU=6 - ICPU=3
- NO WMAP - LARREQUERY - NGG_SCORES=0 - WAIT - DSPELOCK=100 - LONGLOG
- DST TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPEXT=0.5 - FGAPOP=6
- DST TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPEXT=7
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                                                                                                                                                              6, 2004, 10:55:53 ; Search time 104 Seconds (without alignments) 12396.225 Million cell updates/sec
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                   - protein search, using frame_plus_n2p model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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CGAGCCCCTGTGGCCCAGACTTCCCGGAATGTATGAATTCGTGGGATTGGAATTCTTGCCC 1027
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                                    PheGluvalvalGluLysAlaCysArgSerTyrSerHisValValLeuLysGluValArg
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TTTGAGGTGGTGGAGAAGGCCTGCCGCTCCTACAGCCACGTGGTGCTCAAGGAGGTGCGC
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Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Sugain S., Ishii S., Kawai-Hio Y., Saito K., Suzamatui Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamateu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.; Sasaki N., "NEDO human cDNa sequencing project "; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO4746; BAC1177.1; -- Genew, HGNC:1972; CHST4.

Gonew, HGNC:1972; CHST4.

InterPro; IPRO00863; Sulfotransferase activity; IEA.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein FLJ90265.
Hypothetical protein FLJ90265.
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                      "Chromosomal Localization and Genomic Organization for t Galactose/N-Acetylgalactosamine/N-Acetylglucosamine 6-O-Sulfotransferase Gene Family.";
Glycobiology 0:0-0(2001).
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                                                                                                                     321 HisThrAsnAlaArgAspAlaLeuAsnValSerGlnAlaTrpArgTrpSerLeuProTyr
                                                                                                                                                                        GAAAAGGITTCTCGAACTTCAGAAAGCCTGTGGCGATGCCATGAATTTGCTGGGCTACCGC
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Q8IV46;
Q1-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to carbohydrate (N-acetylglucosamine 6-0) sulfotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ dat
EMBL; EG032582; AAH3552B1;
GO:0000146; F:sulfotransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR001092; HILL basic.
InterPro; IPR001083; Sulfotransferase.
PF00685; Sulfotransferase.
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SEQUENCE 386 AA; 45160 MW; 861869348319E42A
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                                                                         CCCCGGAGACAGTCCAGCCTCTTTCAGTGGGAGAACAGCCGGGCCCTGTGTTCTGCACCT
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              HisValTrpMetThrPheLysGlnSerThrAlaTrpMetLeuHisMetAlaValArgAsp
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OFRII;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
L-selectin ligand sulfotransferase.
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Best Local Similarity:
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STRAIN=C57BL/6; TISSUB=Tonail;
MEDLINE=99264336; PubMed=10330415;
MEDLINE=99264336; PubMed=10330415;
Bistrup A., Bhakra S., Lee J.-K., Belov Y.Y., Gunn M.D., Zuo F.-R.,
Huang C.-C., Kannagi R., Rosen S.D., Hemmerich S.;
"Sulfortransferases of two specificities function in the reconstitution of high endothelial cell ligands for L-selectin.";
J. Cell Biol. 145:899-910(1999).
                                                                                                                                                                                                                                                                                                                <u> ATCCAGTCCTTGCCCAAGGCCCTGCAGGAACGCTACCTGCTTGTGCGCTATGAGGACCTG</u>
                                                                                                                                                                                                                                                                                                                                                                                          GCTCGAGCCCCTGTGGCCCCAGACTTCCCGGAATGTATGAATTCGTGGGATTGGAATTCTTG
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1993 (TrEMBLrel. 24, Last annotation update)
01-NOT-203 (TrEMBLrel. 24, Last annotation update)
01-AUN-203 (TrEMBLrel. 24, Last annotation update)
01-AUN-203 (TrEMBLrel. 24, Last annotation update)
04-Keratan) sulfotransferase 4).
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SEQUENCE FROM N.A.

STRAIR-STSTBL/60; TISSUB=TONGUE;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Kawai J., Shinagawa A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Saito T., Matsuda H.A., Ashburner M., Bartalov S., Casawant T.,

Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.
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EMBL, AR13136; AAD33016.1; -.

EMBL, AR09113; BAB26078.1; -.

EMBL, AR09113; BAB26078.1; -.

ROJ GO:0016740; F:tansferase activity; IEA.

GO; GO:0016740; F:tansferase activity; IEA.

Manner, PROG855; Sulfotransferase.
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Conservative:
Mismatches:
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                                                               359 LeuGlnValArgSerGlnGlnGlnGlnGlyAsnLeuserLeuAspLeuLeuSerSerSer 378
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ATCGTGCACCTGGTCCGGGACCCCCGGGCCGTGTTCCGTTCCGAGAACGCACAAAGGGA 784
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                                                GATCTCATGATTGACAGTCGCATTGTGATGGGGCAGCATGAGCAAAAACTCAAGAAGGAG
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MEDILINB-2040230; PubMed=11017086;
MEDILINB-20402330; PubMed=11017086;
Akama T.O., Nishida K., Nakayama J., Matanabe H., Fujiwara T.,
Nakamura T., Dota A., Kawasaki S., Inoue Y., Maeda N., Yamamoto S.,
Ozaki K., Kinoshita S., Shimomura Y., Tanigami A., Fukuda M.N.;
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mutations in a new sulphotransferase gene.";
Nat. 26:237-241(2000).
EMBL; AF219990; AAG26325.1; -.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Hemmerich S., Lee J.-K., Bhakta S., Bistrup A., Ruddle N.R.,
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01-MRA-2001 (TrEMBLrel. 16, Created)
01-MRA-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
N-acetylglucosamine 6-0-sulforransferase GST-4beta (Corneal
N-acetylglucosamine-6-0-sulfotransferase).
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EMBL; AF219991; AAGZ6327.1; -.
Genew; HGNC:6938; CHST6.
GO; GO:01005794; C:GG1g1 apparatus; TAS.
GO; GO:0101517; F:N-acetylglucosamine-6-O-sulfotransferase ac. ..; TAS.
GO; GO:01526; P:proteoglycan sulfate transfer; TAS.
InterPro; IRR008863; Sulfotransferase.
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                               TTGCTGGGCTACCGCCACGTCAGATCTGAACAAGAACAGAAACCTGTTGCTGGATCTT
AlaThrLeuLysPro---ProProPheLeuArgGlyArgTyrArgLeuValArgPheGlu
                                                                                                   ---GACCACGCTTTCCACACACAAATGCCCAGGGATGCCCTTAAATGTCTCCCAGGCTTGGCGC
                                                           1019 ITCTTGCCCCATCTTCAGACCTGGGTGCATAACATCACCCGAGGCAAGGGCATGGGT---
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STRAIN-C57BL/6; TISSUE-Intestine;
MEDLINE-9421499; PubMed=10491328;
MEDLINE-9421499; PubMed=10491328;
Lee J.-K., Bhakta S., Roden S.D., Hemmerich S.;
"Cloning and Characterization of a Mammalian N-Acetylglucosamine-6-Sulfortansferase that is Highly Restricted to Intestinal Tissue.";
Biochem. Biophys. Res. Commun. 263:543-549(1999).
EMBL; AF176840; AAD56002.1; -.
EMBL; AF176840; AAD56002.1; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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GO; GO:0008146; F:sulfotransferase activity;
GO; GO:0016740; F:transferase activity; IEA.
Interbro; IPR000863; Sulfotransferase.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence
01-UW-2003 (TrEMBLrel. 24, Last annotatian Arcetylglucosamine 6-0-sulfotransferase, CHSTS OR I-GLCNAC-6-ST.
Mus musculus (Mouse).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 16, Last sequence update)
101-UTN-2003 (TrEMBLrel. 24, Last sequence (Incestinal N-acetylglucosamine-6-0-sulfotransferase)
101-MAR-2001 (TrEMBLRel. 24, Last sequence (Incestinal N-acetylglucosamine 6-0-sulfotransferase)
101-MAR-2001 (TrEMBLRel. 24, Last sequence (Incestinal N-acetylglucosamine 6-0-sulfotransferase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Macular corneal dystrophy type I and type II are caused by distinct mutations in a new sulphotransferase gene.";
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MEDLINE=99423499; PubMed=10491328;
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EMBL; AF246718; AAG26023.1.
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EMBL; AF176839; AAD556001.1;
EMBL; AF176839; AAD560001.1;
EMBL; AF176839; AAD560001.1;
                                                     1253 CTGTCTACCT---GGACTGTCCCTGAGCAAATCCACTAAGAGGGTTGAGAAG 1301
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                    411 AA; 46160 MW; 97642D54BE926E06 CRC64
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GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0008146; F:sulfotransferase activity; IEA.

GO; GO:00016740; F:transferase activity; IEA.

GO; GO:0006477; P:protein amino acid sulfation; TAS.

InterPro; IPR000863; Sulfotransferase.

Transferase.
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Query Match:
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                                    79 GlyGlnLeuPheSerGlnHisProAspValPheTyrLeuMetGluProAlaTrpHisVal
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SEQUENCE TISSUE=Embryo;

X MEDINE=21085660; PubMed=11217851;

X Eawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Shibata K., Xonno H., Adachi J., Fukuda S.,

Alzawa K., Izawa M., Nishiah K., Kiyosawa H., Kondo S., Yamaraka I.,

Balzawa K., Izawa M., Nishiah K., Kiyosawa H., Kondo S., Yamaraka I.,

Balzawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Blake J., Boffelli D., Bojunga N., Anno H., Baldarelli R., Barsh G.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

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Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamcto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Hyasshizaki Y., Poschida K., Hasegawa Y., Kawaji H., Kohteuki S.,

Hayashizaki Y., Poschida K., Hasegawa Y., Kawaji H., Kohteuki S.,

Hyasshizaki Y.,
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OGT-2003 (TrEMBLrel. 25, Last amoutation update)
01-OGT-2003 (TrEMBLrel. 25, Last amoutation update)
N-acetylglucosamine 6-O-sulfotransferase GST-5 (N-acetylglucosamine-6-O-sulfotransferase) (2600013M07Rik protein) (Carbohydrate
(N-acetylglucosamino) sulfotransferase 7).
CHST7 OR GST5 OR 2600013M07Rik.
Bukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
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TISSUE-Kidney;
Strausberg R.;
Strausberg R.;
Submitted (IBC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR280089; AAG48247.1;
EMBL; AR280089; AAG48247.1;
EMBL; AR011202; BAB27465.1;
EMBL; BC019204; AAH19204.1;
EMBL; BC019204; AAH19204.1;
EMBL; BC019204; AAH19204.1;
EMBL; BC019204; AIL STRAUSPERSE SULFORTANTERSE.

GO; GO:0005406; F:sulfotransferase.

Rema; PF00685; Sulfotransferase.
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Uchimura K., Muram
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PubMed=10956661;
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Length: Matches: Conservative: Mismatches:

1.71e-45 632.50 48.50% 33.26%

Percent Similarity: Best Local Similarity:

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'n	253	CATGCACGTGCTC	SGTTCTGTCTTC	CATGCACGTGCTGGTTCTGTCTGGCGCTCTGGCTCTTTTTGTGTGGGGCAGCTTTTT	CTTCTTTTGT	GGGGCAGCTTTT 31	7
дg	66	: ::: sGlnHisIleTy	rvalHisAlaTh	: rTrpArgThrGlyS	erSerPhele	uGlyGluLeuPh 11	o,
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qq	199	eCysSerProPro	oleuCysProAl	aAlaProArgAlaA	rgAlaAspVa	alGlyLeuValGl 21	ο.
à	571	CCGGGCTCACTG	CAGGCTCCTGTG	CCGGGGCTCACTGCAGGCTCCTGTGCAGTCAACAGCCCTTTGAGGTGGTGGAAAGGCCTG	TTGAGGTGGT	GGAGAAGGCCTG 63	0
Dp	219	uAspLysAlaCy	 	uAspLysAlaCysGluSerThrCysProProValSerLeuArgAlaLeuGluAlaGluCy	euArgAlaLe	uGluAlaGluCy 23	9
ò	631	CCGCTCCTACAG	CCACGTGGTGCT	CCGCTCCTACAGCCACGTGCTCAAGGAGGTGCGCTTCTTCAACCTGCAGTCCCTCTA	TCTTCAACCT	9	06
qa	239	 SArgLysTyrPr	ovalvalvalil	.	euleuAsple	2	59
ò	691	CCCGCTGCTGAA	AGACCCCTCCCT	CCCGCTGCTGAAAGACCCCTCCTCAACCTGCATATCGTGCACCTGGTCCGGGGACCCCG	TGCACCTGGT	7	20
qq	259		gAspProGlyLe	uAsnLeuLysvalV	alGlnieuPh	neArgAspProAr 27	6
ò	751	GGCCGTGTTCCG	TTCCCGAGAACC	GGCCGTGTTCCGTTCCCGAGAACGCACAAAGGGAGATCTCATGATTGACAGT	TCATGATIGA	1 1 1 1 1 1	802
QQ Q	279	gAlaValHisAs	 nSerArgLeuLy	sserArgGlnGlyL	euLeuArgGl	IleGlnVa 2	66
δ	803	1			TTGTGATG	8	14
qq	299	lleuArgThrAr	gGlnArgGlyAe	pHisPheHisArgV	alLeuLeuAl	alAs 3	19
È	815	99	GCAGCATGAGCA		AGGACCAACC	60	n O
qq	319	pAlaArgProGl	yGlyGlnAlaAi	gAlaLeuProSerA	laProArgAl	m	33
È	860	GTGAT	GCAGGTCATCTC	GIGATGCAGGTCATCTGCCAAAGCCAGCTGGAGATCTACAAGACCATCCAGTC	AGATCTACA	9	12
Q	339	uThrSerAlaLe	uGluValileCy	sGluAlaTrpieu	rgAspLeule	m	59

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1033 TCAGACCTGGGTGCATAACATCACCCGAGGCAAGGCATGGGT---GACCACGCTTTCCA 1089
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                                                                                                                                                                                          319 pAlaArgProGlyGlyGlnAlaArgAlaLeuProSerAlaProArgAlaAspPhePheLe 339
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                                                                                                                                                                                                                                        313 TGGGCAGCACCCAGATGTTTTCTACCTGATGGAGCCCGCCTGGCACGTGTGGATGACCTT 372
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                                                                                                                          55 SerLeuGluAlaAlaAlaAlaGlyGluArgGluGlnGlyAlaGluValArgSerLeuAla 74
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279 gAlaValHisAsnSerArgieuLysSerArgGlnGlyLeuLeuArgGluSerIleGlnVa
                                   133 ACTGCCTAAAAAATGAAGCTCCTGCTGTTTCTGGTTTCCCAGATGGCCATCTTGGCTCT
                                                                    75 -----GluGlyAsnProAspArgSerProGlySer
                                                                                                    193 ATTCTTCCACATGTACAGCCACACACATCAGCTCCCTGTCTATGAAGGCACAGCCCGAGCG
                                                                                                                                                                                                                                                                                                                                                                              433 CTTGTGCGACATGAGCGTCTTTGATGCCTACATGGAACCTGGTCCCCGGAGACAG----
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                                                                                                                                                                                                                                                                                                             373 CAAGCAGAGCACCGCCTGGATGCTGCACATGGCTGTGCGGGGATCTGATACGGGCCGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 aProAspSerAlaAsnLeuThrThrAlaMetLeuPheArgTrpArgThrAsnLysValIl
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                                                                                                                                                                                                                         TACGGAAGACGACAGAAGGGTAGAGAAAAAGCGCATGGCCCGG---CTAGCAGTG---
                                                                                         1033 TCAGACCTGGGTGCATAACATCACCCGAGGCAAGGGCATGGGT---GACCACGCTTTCCA
                                                                                                                                                                   399 uAspAlaPheAlaPheAsnMetThrArgGlySerAlaTyrGlyAlaAspArgProPheHi
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Kitagawa H., Uyama T., Sugahara K.;
Kitagawa H., Uyama T., Sugahara K.;
Kitagawa H., Uyama T., Sugahara K.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB046229; BA840372.1; -BBL/GenBank/DDBJ databases.
EMBL; JC7350, JC77350;
MDJ; MGJ; 1891767; Chst7.
GO; GO:0016740; Fitansferase activity; IEA.
GO; GO:0008446; F:sulfotransferase activity; IEA.
HINEAPO; IPR000863; Sulfotransferase.
Ffam; PF00685; Sulfotransferase.
Transferase.
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Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chondroitin 6-Sulfotransferase-2.
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318 sGlyValGlyAlaArgProGlyGlyGlnSerArgAlaLeuProAlaAlaArgAlaAs
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AlaAlaGluGluGlyGlyAlaAsnGlnSerProArg-
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90 SerGlyAlaValGlyGluAlaVal-SerArg----
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                                         075667;
01-NOV-1998 (TEMBLrel. 08, Last sequence update)
01-NOV-1998 (TEMBLrel. 08, Last sequence update)
01-NOV-1998 (TEMBLrel. 25, Last annotation update)
01-OCT-2003 (TEMBLrel. 25, Last annotation update)
N-acetylglucosamine-6-0-sulfotransferase (Carbohydrate
(N-acetylglucosamine 6-0) sulfotransferase 7).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB040711; BAB13770.1; -.
PERL; JC7351; JC7351.
Genew; HGNC:13817; CHST7.
GO; GO:0008146; F:Sulfotransferase activity; IEA.
GO; GO:016740; F:transferase activity; IEA.
FEAM; PF00685; Sulfotransferase.
FEAM; PF00685; Sulfotransferase.
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Uchimura K., Muramatsu T.;
Uchimura K., Muramatsu T.;
"Identification and molecular characterization of a cDNA novel N-acety1glucosamine-6-0-sulfotransferase.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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|SerGlyAlaValGlyGluAlaVal-SerArg------------------------
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53 GlyValTrpSerLeuGluAlaAlaAlaAlaGlyGluArgGluGlnGlyAlaGluAlaArg
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                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-07T-2000 (TYEMBLrel. 15, Last sequence update)
01-07M-2003 (TYEMBLrel. 24, Last annotation update)
01-07M-2011 6-sulfotransferase-2
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                                                                           PRELIMINARY;
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Percent Similarity:
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Query Match:
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                                                                                                                          Homo sapiens (Human)
                                                                                                                                                          SEQUENCE FROM N.A. TISSUE=Brain;
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318 sGlyValGlyAlaArgFroGlyGlyGlyGlnSerArgAlaLeuProAlaAlaArgAlaAs
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GAACGCACAAAGGGAGATCTCATGATTGACAGTCGCATTGTGATG
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                                                                                                         Uchimura K., Muranatsu H., Kadomatsu K., Fan Q., Kurosawa N.,
Whisuoka C., Kannagi R., Habuchi O., Muramatsu T.;
Mutsuoka C., Kannagi R., Habuchi O., Muramatsu T.;
Mutsuoka C., Kannagi R., Habuchi O., Muramatsu T.;
Mudleular cloning and characterization of an N-acetylglucosamine-6-0-
sulfotransferase.",
J. Biol. Chem. 273:22577-22583 (1998).
EMBL; ABO11452; BAA32138 1;
EMBL; ABO11452; BAA32139 1;
EMBL; ABO11451; BAA32137 1;
MGD; WOI:1891160; Chst2.
GO; GO:0008146; F:sulfotransferase activity; IDA.
InterPro; IPR000863; Sulfotransferase.
Fransferase:
Transferase:
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| LysCysProProGlnArgLeuAlaArgPheGluGluGluCysArgLysTyrArgThrVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCCTCAACCTGCATATCGTGCACCTGGGACCCCCGGGCCGTGTTCCGTA
                                    Mus musculus (Mouse).
Wataryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                530 AA; 57814 MW; A113E1B735C363EC CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) N-acetylglucosamine-6-O-sulfotransferase long form.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                        TISSUE=Embryo;
MEDLINE=98380482; PubMed=9712885;
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598.50
54.40%
36.81%
15.99%
                                                                                SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.

SEQUENCE FROM IN.A.

STRAIN=25388257; PubMed=12477932;

STRAIN=25388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

REDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B.B., Bangner L., Shammen C.M., Schuler G.D.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haiseh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiseh F.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan F.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzuy D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Sheychenko Y., Boutfard G.G.,

Blacealey R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rachiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Q80WV3;
Q80WV3;
Q1-UTN-2003 (TrEMBLrel. 24, Created)
Q1-UTN-2003 (TrEMBLrel. 24, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to carbohydrate (N-acetylglucosamine-6-0) sulfotransferase
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                         CITITITGGGCAGCACCCAGAIGITTTCTACCTGAIGGAGCCCGCCTGGCACGTGTGGAIG 367
 Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 LysLeuTyrProGlyAspAlaValSerLeuGlnGlyAlaAlaArgAspMetLeuSerAla
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                                                                                                                                                                                              CRC64;
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                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6, TISSUE=Brain;
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54.40%
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382 GlymetGlyGlyProAlaAspTyrHisAlaLeuGlyAlaMetGluVallleCysAsnSer 401
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                                                                          944 CTTGTGCGCTATGAGGACCTGGCTCGAGCCCCTGTGGCCCCAGACTTCCCGAATGTATGAA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=5606;
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Search completed: May 6, 2004, 11:05:46 Job time : 124 secs

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Glycosyl sulfotransferase; GST-3; detection; diagnosis; leukocyte homing; selectin binding interaction; inflammation; lymphocyte homing; human; secondary lymph organ.
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98US-00190911
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-MODEL=frame+. npp. model - DEV=Xlp
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-MODEL=frame+. npp. model - DEV=Xlp
-DS=A Geneseq_29Jan04 - QPMT=fastan - SUFPIX=rag - MINMATCH=0.1 - LOOPCL=0
-LOOPEXT=O - UNITS=bits - START=1 - SND=-1 - MATRIX=blosum62 - TRANS=human40.cdi
-LIST=45 - DOCALIGN=200 - THR SCORE=pcr - THR MAX=100 - THR MIN=0 - ALIGN=15
-MODE=LOCAL - OUTFMT=pco - NORM=ext - HEAPS/IEE=500 - MINLEN=0 - MAXLEN=200000000
-USER=US09645078 @CGN 1 1 81 @runat - 06052004 104558 21717 - NOPU=6 - ICPU=3
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Aay815640 Human g
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Copyright (c) 1993 - 2004 Compugen Ltd.
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GAAAAGGTTTCTCGACTTCAGAAAGCCTGTGGCGATGCCATGAATTTGCTGGGCTACCGC
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S, Otsuki
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K, Kojima
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Sugiyama T, Nagai
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                                          This sequence is the human glycosyl sulfotransferase-3 (GST-3) of the invention. The nucleic acid sequences, probes and primers derived from these, proteins and antibodies are useful in detecting homologues. The sequences, antibodies and methods are useful in the diagnosis and treatment of diseases associated with selectin binding interactions, including conditions associated with or resulting from the homing of leukocytes to sites of inflammation and the normal homing of lymphocytes to secondary lymph organs
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length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length muman cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New enzyme, useful for modifying acceptor molecule, comprises an isolated L-selectin sulfotransferase-2 that directs expression of L-selectin 11gand antigen, MECA-79 in Chinese hamster ovary cells, or intestinal Glorac 6-sulfotransferase.
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                   221 IleValMetGlyGlnHisGluGlnLysLeuLysLysGluAspGlnProTyrTyrValMet
                                                                        CAGGICATCIGCCAAAGCCAGCIGGAGAICIACAAGACCAICCAGICCIIGCCCAAGGCC
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            directs expression of a MECA-79 antigen. This can be done by directs expression of a MECA-79 antigen. This can be done by directs expression of a MECA-79 antigen. This can be done by administering to the subject an oligoaccharide L-selectin antagonist that inhibits binding of L-selectin to a MECA-79 antigen, for example by administering antibody material that specifically binds betal, 3GT, antisense nucleic acid molecule. L-selectin.

and/or a betal, 3GT antisense nucleic acid molecule. L-selectin.

alternatively, the expression or activity of LSST-2 or its active fragment can be reduced in combination with reducing the expression or activity of betal, 3GT. The method is useful for treating L-selectin mediated conditions such as Crohn's disease and ulcerative colitis, inflammatory disorders of the skin such as allergic contact dermatitis, providensis and Lichen planus, lymphomas, chronic pneumonia, delayed-type hypersensitivity reactions, diabetes and hyperplastic thymus. This
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The present sequence is that of human transferase TRNSFS-11, 1 of 15 claimed novel human transferase proteins of the invention (see AAY79209-31). The sequence was deduced from a cDNA clone (see AAZ94211) isolated from a gallbladder library. It shows homology to mouse Nearatologic and gastrointestinal tissues, especially those associated with inflammation and cell proliferation. The new human transferases and polynuclectides can be used in the diagnosis, prevention and treatment of cancer, developmental disorders, gastrointestinal disorders, genetic disorders, immunological disorders, neurological disorders preproductive disorders, and smooth muscle disorders. The polypeptides can also be used to raise antibodies, and to screen for agonists and antagonists of
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cancers and developmental, gastrointestinal, genetic, immunological
neurological, reproductive and smooth muscle disorders.
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                                           /note= "potential N-glycosylation"
364
/note= "potential O-phosphorylation"
780
/note= "potential O-phosphorylation"
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                'note= "potential N-glycosylation"
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Hillman JL, Azimzai Y;
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11-MAY-1999;
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Length:
Matches:
Conservative:
Mismatches:
Indels: 6.84e - 1681984.00 99.48% 98.97% 53.02% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores:

Sequence 386 AA;

338 338 0 0 0

US-09-645-078-1 (1-2043) x AAY79219 (1-386)

qq	61 LeuPheGlyGlnHisProAspValPheTyrLeuMetGluProAlaTrpHis	/alTrpMet 80
à	368 ACCTTCAAGCAGAGCACCGCCTGGATGCTGCACGTGCTGCT	ATACGGGCC 427
dC	81 ThrPheLysGlnSerThrAlaTrpMetLeuHisMetAlaValArgAspl	eArgala 1
ò	428 GICTICTIGIGGACAIGAGCGICTITGAIGCCIACAIGGAACCIGGIC	CCCGGAGACAG 487
д	101 ValPheLeuCysAspMetSerValPheAspAlaTyrMetGluProGly	ArgArgGln 120
λο i	488 TCCAGC	rereacarc 547
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දු දු	548 AFCCACAAGATGAATGAATGACCCGGGCTCATGCAGGCTCTGTGCAGCTCATGAGCCC 141 IleFroGlnAspGlu-SerSerProGlyLeuThrAlaGlySerCysAlaValAsnSerPr	16
à	608 TTTGAGGTG-GTGGAGAAGGCCTGCCGT	99
q	160 oleulysLeuleuGlulysAlaCysArgSerTyrSerHisValValLeulysGluValAr	Н
\$ B	667 CTICTICAACCIGCAGICCCTCAACCGCTGCTGAAAGACCCCTCCCTCAACCT	CCTGCATAT 726
ò	727 CGTGCACCTGGTC	GGGAGA 78
d d	_ 500 500 6	
ò	787 TCTCA:	ω .
g G	220 p	24
ò	847 CCAACCCTACTATGTGATGCAGGTCATCTGCCAAAGCCAGCTGGAGA	0
qq	240 pGlnProTyrTyrValMetGlnValIleCysGlnSerGlnLeuGluI	1 26
ð i	907	φ (
d d	260 eGlnSerI	premal 280
හි සි	967 TCGAGCCCTGTGGCCCAGACTTCCCGAATGTATGAATTCGTGGAATTGAATTC	ATTCTTGCC 1026 uPheLeuPr 300
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δ	1087 CCACACAAATGCCAGGGA	TTTGCCCTA 1146
d	320 eHisThrAsnAlaArgAspAlaLeuAsnValS	rLeuProTy 340
ò	1147 IGAAAAGGITICICGACITICAGAAAGCCIGIGGCGAIGCCAIGAAITIGCIGGG	CTACCG 12
ద	340 rGluLysValSerArgLeuGlnLysAlaCysGlyAspAlaMetAsnLeuL	uglytyrar 360
ζ	1207 CCAGGTCAGATCTGAACAAAAAAGAAAACCTGTTGCTGGATCTTCTGT	CTGGAC 12
q	360 gHisValargSerGluGlnGlnGrgAsnLeuLeuLeuAspLeuLeuS	- [-
ò	/ 1267 IGTCCCTGAGCAAATCCAC 1285	
q	380 rValProGluGlnIleHis 3	
RESU AAY3 ID	JLT 5 39919 AAY399	
X X X	AAY3991	
점	r 08-DEC-1999 (first entry)	

364 247 304 ATGACCTTCAAGCAGAGCACCGCCTGGATGCTGCACATGGCTGTGCGGGATCTGATACGG 424 78 98 This sequence is the mouse glycosyl sulfotransferase-3 (GST-3) of the invention. The nucleic acid sequences, probes and primers derived from these, proteins and antibodies are useful in detecting homologues. The sequences, antibodies and methods are useful in the diagnosis and treatment of diseases associated with selectin binding interactions, including conditions associated with or resulting from the homing of leukocytes to sites of inflammation and the normal homing of lymphocytes to secondary lymph organs 38 80 sulfotransferase; GST-3; detection; diagnosis; leukocyte homing; binding interaction; inflammation; lymphocyte homing; mouse; lymph organ. 20 Human and murine glycosyl sulfotransferase 3 and related polynucleotides. ATGCTACTGCCTAAAAAATGAAGCTCCTGCTGTTTCTGGTTTCCCAAGATGGCCATCTTG GAGCGC - - - ATGCACGTGCTGGTTCTTCCTGGCGCTCTGGCTCTTTTGTGGGG CAGCITITIGGGCAGCACCCAGAIGITITICIACCIGAIGGAGCCCGGCCTGGCACGIGIGG GCTCTATTCTTCCACATGTACAGCCACACATCAGCTCCCTGTCTATGAAGGCACAGCCC # 2 4 2 2 2 8 8 2 2 8 2 2 2 sulfotransferase-3 protein sequence ŝ Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: Hemmerich (1-388)Ж, Tangemann US-09-645-078-1 (1-2043) x AAY39919 2; Fig 4; 59pp; English 1.98e-126 1519.50 85.13% 72.56% 98US-00045284. 99WO-US004316 (REGC) UNIV CALIFORNIA. Bistrup A, Rosen SD, WPI; 1999-580442/49. N-PSDB; AAZ20793. Percent Similarity: Best Local Similarity: Glycosyl sulfotra selectin binding secondary lymph c Ä glycosyl Sequence 388 20-MAR-1998; 12-NOV-1998; Alignment Scores: 26-FEB-1999; WO9949018-A1 30-SEP-1999 48 128 Н 188 21 39 305 9 365 79 Query Match: DB: Claim .. 90 Mouse à 임 ठे g Š d à В ℅

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GCCGTCTTCTTGTGCGACATGAGCGTCTTTGATGCCTACATGGAACCTGGTCCCCGGAGA

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CGCCACGTCAGATCTGAACAAAAACAGAAACTGTTGCTGGATCTTCTGTCTACCTGG 1264
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                                                                                   ATCATCCCACAAGATGAAATCATCCCCCGGGCTCACTGCAGGCTCCTGTGCAGTCAACAG
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                                                                                                                          PhephebroAlaHisGluIleSerSerProLysHisCysLysLeuLeuCygGlyGlnGln
                                                                                                                                                                              CCCTTTGAGGTGGAGAAAGGCCTGCCGCTCCTACAGCCACGTGGTGCTCAAGGAGGTG
                                                                                                                                                                                                         CGCTTCTTCAACCTGCAGTCCCTCTACCCGCTGCTGAAAGACCCCTCCAACCTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                     GATCTCATGATTGACAGTCGCATTGTGATGGGGCAGCATGAGCAAAAAACTCAAGAAGGAG
CAGTCCAGCCTCTTTCAGTGGGAGAACAGCCGGGCCCTGTGTTCTGCACCTGCTGTGAC
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SerValPheLeuCysAspMetSerValPheAspAlaTyrMetAsnProGlyProArgLys

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antianaemic, gene therapy, concer, proliferative disorder; hypertension, neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; pyrothyroidism; SCID; ALDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; thrombosis; contraceptive.
antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
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Homo sapiens.

WO200058473-A2.

05-OCT-2000.

31-WAR-1999; 99US-0127607P. 02-APR-1999; 99US-0127636P. 05-APR-1999; 99US-0127728P. 30-WAR-2000; 2000US-00540763. 31-MAR-2000; 2000WO-US008621.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

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WPI; 2000-602362/57. N-PSDB; AAC76156. Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.

Claim 11; Page 2599-2600; 5507pp; English.

AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic, hepatotropic; vulnerary; sequences have activities such as: cytostatic, hepatotropic; vulnerary; antipartiant; limituparkinsonian; nootropic; neuroprotective; osteopathic; cardiant; thrombolythic; coaquiant; vasotropic; antipabetic; hypotensive; cardiant; thrombolythic; coaquiant; vasotropic; antipabeterial; properties antivity antibacterial; antivity antibacterial; antivity antibacterial; antivity antibacterial; antivity antibacterial; antivity antibacterial; antivity an be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, cardiovascular disease, disorders, osteoarthritis, graft vs host disease, cardiovascular disease, disorders, systemic lupus erythematosus, severe combined immunodeficiency (SCID) AIDS, viral, bacterial or fungal infection, malaria, autoimmune catiloge damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive

Sequence 418 AA;

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418	249	54	85	49	10
Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
1.176-98	1208.50	69.34%	56.98%	32.30%	3
Alignment Scores: Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

GACAGAAGGGTAGAGAGAAAAGCGCA-----TGGCCCGGCTAGCAGTGAGCCTCT 79 US-09-645-078-1 (1-2043) x AAB41947 (1-418) 59 10

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419	TTGTGGGACATGAGCGTCTTTGATGCCTACATGGAACCTGGTCCC 47.
479	CCAGTGGGAGAACAGCCGGGCCCTGTGTTCTGCACCTGCC 5
539	GAAATCATCCC
599	CAACAGCCCTTTGAGGTGGTGGAGAAGGCCTGCCGCTCCTACAGCCACGTGGTGGTCAAG 658
659	GAGGTGGGCTTCTTCAACCTGCAGTCCCTCTACCCGCTGCTGAAAGACCCCTCCCT
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779	3GGAGATCTCATGATTGAGAGGGGGGGGAGCATGAGAAAACTCAAG 8
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953	TATGAGGACCTGGCTCGAGCCCCTG] :::
1013	TIGGAATICTIGCCCCATCTICAGACCTGGGTGCATAACAICA
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1127	TGGCGCTGGTCTTTGCCCTATGAAAAGGTTTCTCGACTTCAGAA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding corneal N-acetylglucosamine-6-sulfotransferase useful for treatment, monitoring and diagnosis of macular corneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes human corneal N-acetylglucosamine-6-sulforransferase (I), which is able to catalyse sulfation of keratan sulfate (KS). Also described is a method for monitoring the effect of treatments for macular corneal dystrophy (MCD), and detecting associptibility to MCD. (I) is located to chromosome 1622, and has ophthalmological activity. (I) can be used to treat or prevent macular corneal dystrophy types I or II. (I) makes possible treatment of MCD without requiring keratinoplasty or keratectomy. The present sequence represents mouse intestinal N-acetylglucosamine-6-sulfotransferase, which is given in comparison with (I) in the exemplification of the
                                             Human, N-acetylglucosamine-6-sulfotransferase, enzyme, GlcNAc6ST,
corneal, sulfation, keratan sulfate, macular corneal dystrophy, MCD,
                                                                                                                                                                                                         intestinal N-acetylglucosamine-6-sulfotransferase SEQ ID NO:5
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| AspleuValLeuProArgGlyProAspHisPheSerTrpAlaSerProAsp
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11-AUG-2000; 2000US-0325773P.
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(AKAM/) AKAMA T O.
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ophthalmological
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Length:
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9.076-83 1030.50 66.75% 55.67% 27.54%

Percent Similarity: Best Local Similarity:

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Best Local S. Query Match:

(1-418)

US-09-645-078-1 (1-2043) x ABB81557

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                            398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; selectin binding inhibitor; gene therapy; inflammation; systemic lupus erythematosus; SLB; rheumatoid arthritis; diabetes; polyarteritis nodosa; polymyositis; systemic sclerosis; dermatitis; glomerulonephritis; myasthenia gravis; Sjogren's syndrome; adrenalitis; Hashimoto's disease; Grave's disease; hypoparathyroidism; anaemia; demyelinating disease; cirrhosis; ulcerafive colitis; allergic rhinitis; myocarditis; adult respiratory distress syndrome; eczema; psoriasis; asthma; hypersensitivity; rheumatic fever; tissue rejection;
glycosyl sulfotransferase-4beta; GST-4beta; immunosuppressive;
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                                                                               1256 TCTACCT---GGACTGTCCCTGAGCAAATCCACTAAGAGGGTTGAGAAG 1301
                                                                                                                 Human glycosyl sulfotransferase-4beta (GST-4beta).
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|ThrAlaLeuLeuLeuAlaGlnThrPheLeuLeuLeuPheLeuValSerArgPro----
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256 AlaThrLeuLysPro---ProProPheLeuArgGlyArgTyrArgLeuValArgPheGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---GACCACGCTTTCCACACAAATGCCAGGGATGCCCTTAATGTCTCCCAGGCTTGGCGC
                                                                                                                                                                                                                545 ATCATCCCACAAGATGAAATCATCCCCCGGGCTCACTGCAGGCTCCTGTGCAGTCAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       605 CCCTTTGAGGTGGTGGAGAAGGCCTGCCGCTCCTACAGCCACGTGGTGCTCAAGGAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .019 TTCTTGCCCCCATCTTCAGACCTGGGTGCATAACATCACCGGGGGCAAGGCCATGGGT---
 Mismatches:
Indels:
                                  Gaps:
                                                            (1-395)
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 53.98% 27.49%
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                                            TGGTCTTTGCCCTATGAAAAGGTTTCTCGACTTCAGAAAGCCTGTGGCGATGCCATGAAT 1192
                                                                                                                                                                  CTGTCTACCTGGACTGTCCCTGAGCAAATCCACTAAGAGGGTTGAGAAGGCTTTGCTGCC 1312
                                                                                                                                    355 LeuLeuGlyTyrArgProValTyrSerGluAspGluGlnArgAsnLeuAlaLeuAspLeu 374
315 ArgArgGluAlaPheLysThrSerSerArgAsnAlaLeuAsnValSerGlnAlaTrpArg 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding corneal N-acetylglucosamine-6-sulfotransferase, useful for treatment, monitoring and diagnosis of macular corneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents human corneal N-acetylglucosamine-6-sulforransferase (I), which is able to catalyse sulfation of keratan sulfate (KS). Also described is a method for monitoring the effect of treatments for macular corneal dystrophy (MCD), and detecting susceptibility to MCD. (I) is located to chromosome 1692, and has substantial dystrophy types I or II. (I) makes possible treatment of MCD without requiring keratinoplasty or keratectomy
                                                                 :::||||||::: |||||::: |||:::||||:::|||| HisAlaLeuProPheAlaLysIleArgArgValGInGluLeuCysAlaGlyAlaLeuGln
                                                                                                       TTGCTGGGCTACGCCACGTCAGATCTGAACAAGAACAGAGAAACCTGTTGCTGGATCTT
                                                                                                                                                                                       375 Val------LeuPro-------ArgGlyLeuAsnGlyPhe-----
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; N-acetylglucosamine-6-sulfotransferase; enzyme; GlcNAc6ST; corneal; sulfation; keratan sulfate; macular corneal dystrophy; MCD; ophthalmological; chromosome 16q22.
                                                                                                                                                                                                                                                                                                                                                                                                                Human corneal N-acetylglucosamine-6-sulfotransferase SEQ ID NO:2.
                                                                                                                                                                                                                             1313 ACCTGGTGTCAGCCTCAGTCACTTTCTCTGAATGCTTCTGAGCCT 1357
                                                                                                                                                                                                                                                    |||
-----SerSerThrAlaSerHisPro 393
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                                                                                                                                                                                                                                                                                                                       ABB81554 standard; protein; 395
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                                                                                                                                                                                                                                                           384 ThrirpAla---
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N-PSDB; ABN89506.
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(AKAM/) AKAMA T O.
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      1133 TGGTCTTTGCCCTATGAAAAGGTTTCTCGACTTCAGAAAGCCTGTGGCGATGCCATGAAT 1192
                                                                                          CTGTCTACCTGGACTGTCCCTGAGCAAATCCACTAAGAGGGTTGAGAAGGCTTTGCTGCC 1312
                     Novel isolated human drug metabolizing enzymes referred as DME 1-10, useful for diagnosing, treating, or preventing disorders associated with
                                                                                                                                                                                                                                                                                 Human; drug metabolising enzyme; gene therapy; autoimmune disorder; inflammatory disorder; acquired immune deficiency syndrome; infection; AIDS; adult respiratory distress syndrome; cell proliferative disorder; allergy; anaemia; conjunctivitis; actinic keratosis; arteriosclerosis; cancer; endocrine disorder; hypothalamus disorder; pituitary disorder; gastrointestinal disorder; metabolic disorder; developmental disorder; liver disorder; iritis; cystic fibrosis; Addison's disease; retinitis; goitre; diabetes; depabagia; gastric carcinoma; anorexia; eye disorder;
                                                              375 Val------LeuPro------ArgGlyLeuAsnGlyPhe----
                                                 TTGCTGGGCTACCGCCACGTCAGAACAAGAACAGAAAACCTGTTGCTGGATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Policky JL, Hafalia A, Burford N, Ring HZ, Lal P, Tribouley CM; Yao MG, Yue H, Tang YT, Patterson C, Das D, Sanjanwala MS; Gandhi AR, Reddy R, Khan FA, Baughn MR, Ramkumar J, Griffin JA; Au-Young J;
                                                                                                                                   ACCTGGTGTCAGCCTCAGTCACTTTCTCTGAATGCTTCTGAGCCT 1357
                                                                                                                                                        ----SerSerThrAlaSerHisPro 393
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/label= Signal_peptide
33. .395
/note= "Human mature DME-5 protein"
36. .395
/note= "Human mature DME-5 protein"
                                                                                                                                                                                                                                                             Human drug metabolising enzyme (DME)-5

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                                                                                                                                                                                                AAE15438 standard; protein; 395
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19-APR-2000; 2000US-0198403P.
28-APR-2000; 2000US-0200185P.
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2000US-0203509P
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N-PSDB; AAD24670.
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The invention relates to human drug metabolising enzymes referred as DME and nucleic acid molecules encoding such enzymes. Polynucleotides of the invention are useful incr assessing toxicity of test compounds and in gene therapy. Sequences of the invention are useful in the diagnosis, cheered therapy. Sequences of the invention are useful in the diagnosis, compounds and in gene therapy. Sequences of the invention are useful in the diagnosis, compounds and in gene prevention and treatment of autoimmune/inflammatory disorders such as addiagnosis, attention anaemia, anaemia, atherosclerosis, asthma, autoimmune deficiency syndrome (AIDS), adult respiratory distress syndrome, allergies, anaemia, atherosclerosis, asthma, autoimmune contentions of the content dermatitis, Crohn's disease, autoimmune contention of the content of the contention of the cont
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aberrant expression of DME such as allergy, anemia, asthma, infertility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 HisAlaLeuProPheAlaLysIleArgArgValGlnGluLeuCysAlaGlyAlaLeuGln 354
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                    AlaPheProArgGlyAlaIleSerSerGluAlaValCysLysProLeuCysAlaArgGln 156
                                                                                  157 SerPheThrLeuAlaArgGluAlaCysArgSerTyrSerHisValValLeuLysGluVal 176
                                                                                                                                                                                                             217 AlaLeuAlaArgAspAsnGlyIleValLeuGlyThrAsnGlyThrTrpVal---GluAla 235
                                                                                                                                                                                                                                                                                                                                           |||
| AspProGlyLeuArgValValArgGluValCysArgSerHisValArgIleAlaGluAla 255
                                                                                                                                                                                                                                                                                                                                                                                      ---ACCATCCAGTCCTTGCCCAAGGCCCTGCAGGAACGCTACCTGCTTGTGCGCTATGAG 958
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                                                                                                                                                                                          ATCGTGCACCTGGTCCGGGGACCCCGGGCCGTGTTCCGTTCCCGAGAAGGCACAAAGGGA 784
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ATCATCCCACAGATGAAATCATCCCCCGGGCTCACTGCAGGCTCCTGTGCAGTCAACAG 604
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RESULT 11

AAY72638

ID AAY72638 standard; protein; 395 AA.

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AAY72638;

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DT 02-MAY-2001 (first entry)

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Mouse; glycosyl sulfotransferase-4 (GST-4).

XX

Mouse; glycosyl sulfotransferase-4; GST-4; immunosuppressive; therapy;

XN

Selectin binding inhibitor; grave; Siz; rheumacidia, diabetes;

XN

Polyarteritis nodosa; polymyositis; systemic sclerosis; dermatitis;

XN

Glomerulonephritis; myssthenia gravis; Sjogren's syndramitis;

XN

Hashimoto's disease; Grave's disease; hypoparathyroidism; anaemia;

KW

demyelinating disease; cirrhosis; ulcerative colitis; allergic rhinitis;

The present sequence is mouse glycosyl sulfotransferase-4 (GST-4). GST-4

Gene is found on chromosome BEI. GST is a type 2 membrane protein useful

C for inhibiting a binding event between a selectin and a selectin ligand,

which comprises contacting the selectin with a non-sulphated selectin

Ilgand, GST and a small molecular agent that inhibits the sulphation

activity of GST. GST is also useful in inhibiting a selectin mediated

binding event. GST is useful in gene therapy to treat disorders such as

acute or chronic inflammation, systemic lupus erythematosus (SLE),

cheumatoid arthritis, polyarteritis nodosa, polymyositis,

dermatomyositis, systemic selerosis, diabetes, glomerilonephritis,

dermatomyositis, systemic selerosis, diabetes, glomerilonephritis,

disease, adrenalitis, hypoparathyroidism, perincious ansemia,

disease, adrenalitis, hypoparathyroidism, perincious ansemia,

myocarditis, regional enteritis, adult respiratory distress syndrome,

infantile eccema, psoriasis lichen planus, allergic rhinitis, bronchial

asthma, hypersensitivity, rheumatic fever and tissue rejection during New glycosyl sulfotransferases (GST)-4alpha, GST-4beta and GST-6 for diagnostic and therapeutic agent screening applications. myocarditis; adult respiratory distress syndrome; eczema; psoriasis; asthma; hypersensitivity; rheumatic fever; tissue rejection; chromosome 8E1. ŝ English Lee JK, Hemmerich 20-JUL-1999; 99US-0144694P. 19-JUL-2000; 2000WO-US019741 (REGC) UNIV CALIFORNIA. Claim 3; Fig 2; 128pp; WPI; 2001-138471/14. N-PSDB; AAD02696. Seguence 395 AA; WO200106015-A1 25-JAN-2001 Rosen SD,

US-09-645-078-1 (1-2043) x AAY72638 (1-395)

395 222 1221 120 130 8

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

7.67e-82 1020.00 66.58% 55.53% 27.26%

Percent Similarity: Best Local Similarity: Query Match: DB:

Alignment Scores:

λ	128 AT	128 AIGCTACTGCCTAAAAAAATGAAGCTCCTGCTGTTTCTGGTTTCCCAGATGGCC 181	.81
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٥٧	182 AT	ζ) υ-	141
Db	21 11	21 IleLeuValPheLeuValSerArgGlnValProSerSerProAlaGly 36	9
δ	242 CA	242 CAGCCCGAGCGCATGCACGTGCTTCTGTCTTCCTGGCGCTCTGGCTCTTCTTTTGTG 301	101
O b	37 Le	37 LeuGlyGluhrgValHisValLeuValLeuSerSerTrpArgSerGlySerSerPheVal 56	9.
ò	302 GG	302 GGGCAGCTTTTTGGGCAGCACCCAGATGTTTTCTACCTGATGGAGCCCGCCTGGCACGTG 361	198
qq	57 G1	57 GlyGlnLeuPheSerGlnHisProAspValPheTyrLeuMetGluProAlaTrpHisVal 76	9,

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Claim 28; Fig 10; 98pp; English.
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          722 CATATCGTGCACCTGGTCCGGGACCCCCGGGCCGTGTTCCGTTCCCGAGAACGCACAAAG
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The present invention provides a method of modifying an acceptor molecule by contacting the acceptor with an isolated betal.3-Notacetylucosaminyltransferase (betal.3GnT) or an active fragment, where betal.3GnT directs expression of a MECA-79 antigen. The invention also provides a method of treating or preventing an L-selectin-mediated condition by reducing the expression or activity of a betal.3GnT that directs expression of a MECA-79 antigen. This can be done by administering to the subject an oligosaccharide L-selectin antagonist that inhibits binding of L-selectin to AMECA-79 antigen, for example by administering antibody material that specifically binds betal.3GnT, and/or a betal.3GnT antisense nucleic acid molecule. L-selectin

Sulfortransferase-2 (LSST-2) also directs MECA-79 antigen expression. Alternatively, the expression or activity of LSST-2 or its active fragment can be reduced in combination with reducing the expression or activity of betal.3GnT. The method is useful for treating L-selectin mediated conditions such as Crohn's disease and ulcerative colitis, inflammatory disorders of the skin such as allergic contact dermatitis, propersensitivity reactions, diabetes and hyperplastic thymus. This sequence represents mouse I-GINNAGST Mouse; betal, 3GnT; betal, 3-N-acetylglucosaminyltransferase; MECA-79; L-selectin; L-selectin sulforransferase-2; Crohn's disease; diabetes; ulcerative colitis; inflammatory skin disorder; psoriasis; Lichen planus; allergic contact dermatitis; lymphoma; chronic pneumonia; LSST-2; delayed-type hypersensitivity; reaction; hyperplastic thymus; antiulcer; antiinflammatory; antipsoriatic; antidiabetic; dermatological; antiallergic; intestinal-GlCNAc 6-sulfotransferase; I-GlCNAc6ST. acceptor molecule, comprises an isolated at directs expression of L-selectin se hamster ovary cells, or intestinal New enzyme, useful for modifying acceptor molecule, comp. L-selectin sulfotransferase-2 that directs expression of ligand antigen, MECA-79 in Chinese hamster ovary cells, GlcMx 6-sulfotransferase.

riginatic Scores; ed. No.: ore: creet Smilarity; st Local Similarity; ery Match: i.09-645-078-1 (1- 128 ATGCT 1 MetAr	lgment Scores: ore: rcent Similarity: ery Match: -09-645-078-1 (1-2043) 128 ATGCTACTG 1 MetArgLeu 1 MetArgLeu 182 ATCTTGGCT	od. No.: 1020.00 Matcl recent Similarity: 6.109-645-078-1 128 ATGCTACTGCTAAAAAAATGAA 1128 ATGCTACTGCTAAAAAAATGAA 1128 ATGCTACTGCTAAAAAAATGAA 1128 ATGCTACTGCTAAAAAAATGAA 1128 ATGCTACTGCTAAAAAAATGAA 1128 ATGCTACTGCTAAAAAAATGAA 1128 ATGCTACTACTGCCTAAAAAAATGAA 1128 ATGCTACTACTACTCCTCAAAAAAATGAAA 1128 ATGCTACTACTACTCCTAAAAAAATGAAA	Length: Matches: Conservative: Mismatches: Indels: Gaps: (1-395) AAATGAAGCTCCTGCTG erThrvalMetLeuSer	Scores: 7.67e-82 Length: 395 1020.00 Matches: 221 1020.00 Conservative: 44 Similarity: 55.53% Mismatches: 120 h: 27.26% Indels: 8 130 078-1 (1-2043) x AAU11275 (1-395) 128 ATGCTACTGCCTAAAAAAATGAAGGTCCTGCTGTTTTCTGGTTTCCCAGATGGCC 181
CVI		; PheL	::: -LeuValSerArgGlnVal	21 IleLeuValPheLeuValSerArgGlnValProSerSerProAlaGly 36

(I-GlcNAc6ST) protein.

intestinal-GlcNAc 6-sulfotransferase

Murine

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ABB81555 standard; protein; 395

ABB8155

(first entry)

05-SEP-2002 ABB81555;

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242 CAGCCCGAGCGCATGCACGTGCTGGTTCTTCCTGGCGCTCTGGCTCTTTTGTG
                                                                    LeuGlyGluArgValHisValLeuValLeuSerSerTrpArgSerGlySerPeVal
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Human, N-acetylglucosamine-6-sulfotransferase; enzyme; GlcNAc6ST;
corneal; sulfation; keratan sulfate; macular corneal dystrophy; MCD;
ophthalmological.
                          Consensus N-acetylglucosamine-6-sulfotransferase SEQ ID NO:3.
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11-AUG-2000; 2000US-0325773P.
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117 LeuSerAspLeuPheGlnTrpAlaValSerArgAlaLeuCysSerProProAlaCysSer 136
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            nucleic acid encoding corneal N-acetylglucosamine-6-sulfotransferase,
                                                                                             The present invention describes human corneal N-acetylglucosamine-6-sulforransferase (I), which is able to catalyse sulfation of keratan sulfate (KG). Also described is a method for monitoring the effect of treatments for macular corneal dystrophy (MCD), and detecting susceptibility to MCD. (I) is located to chromosome 1642, and has ophthalmological activity. (I) can be used to treat or prevent macular corneal dystrophy types I or II. (I) makes possible treatment of MCD withour requiring keratinoplasty or keratectomy. The present sequence represents a consensus N-acetylglucosamine-6-sulforransferase which is given in the exemplification of the present invention
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137 AlaPheProArgGly***IleSerSerGlu***ValCysLysProLeuCysAlaArgGln
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Matches:
Conservative:
Mismatches:
Indels:
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GATCTCATGATTGACAGTCGCATTGTGATGGGGCAGCATGAGCAAAAAACTCAAGAAGGAG
                                                                  LeuThrProGlnLeuGluAlaTrplleHisAsnIleThrHisGlySerGlyProGlyAla
                                                                                                                                                                                                                                                                                 315 ArgArgGluAlaPheLysThrSerSerArgAsnAlaLeuAsnValSerGlnAlaTrpArg
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                                                   GACCAACCCTACTATGTGATGCAGGTCATCTGCCAAAGCCAGCTGGAGATCTACAAG----
                                                                                                         902 ---ACCATCCAGTCCTTGCCCCAAGGCCCTGCAGGAACGCTACCTGCTTGTGCGCTATGAG
                                                                                                                                                                                                                                                                  1076 ---GACCACGCTTTCCACACACAAATGCCAGGGATGCCCTTAATGTCTCCCAGGCTTGGCGC
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13-JUN-2000; 2000US-00593828.
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177 ArgPhePheAsnLeuGlnValLeuTyrProLeuLeuSerAspProAlaLeuAsnLeuArg 196

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ATCGTGCACCTGGTCCGGGACCCCCGGGCCGTGTTCCGTTCCCGAGAACGCACAAAGGGA

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GlnProPheSerLeuAlaArgGluAlaCysArgSerTyrSerHisValValLeuLysGlu 176
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                                                                           New glycosyl sulfotransferases (GST)-4alpha, GST-4beta and GST-6 for diagnostic and therapeutic agent screening applications.
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256 AlaAlaThrLeuLysPro---ProProPheLeuArgGlyArgTyrArgLeuValArgPhe
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corneal; sulfation; keratan sulfate; macular corneal dystrophy; MCD;
ophthalmological.
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Fukuda MN, Akama TO; WPI; 2002-507643/54. dystrophy

177 ValArgPhePheAsnLeuGlnValLeuTyrProLeuLeuSerAspProAlaLeuAsnLeu 196

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722 CATATOGIGCACCIGGICCGGGACCCCCGGGCCGIGITCCGTTCCCGAGAACGCAAAAG

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New nucleic acid encoding corneal N-acetylglucosamine-6-sulfotransferase, useful for treatment, monitoring and diagnosis of macular corneal The present invention describes human corneal N-acetylglucosamine-6-sulforransferase (I), which is able to catalyse sulfation of keratan sulfate (KS). Also described is a method for monitoring the effect of treatments for macular corneal dystrophy (WCD), and detecting susceptibility to MCD. (I) is located to chromosome 16q22, and has ophthalmological activity. (I) can be used to treat or prevent macular corneal dystrophy types I or II. (I) makes possible treatment of MCD without requiring keratinoplasty or keratectomy. The present sequence represents human intestinal N-acetylglucosamine-6-sulfotransferase, which is given in comparison with (I) in the exemplification of the Example 5; Fig 2A-B; 69pp; English.

Sequence 390 AA;

390 206 57 105 7 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 7.32e-81 1009.00 66.41% 52.02% 26.96% Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: Pred. No.:

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ò	662	GTGGGCTTCTTCAACCTGCAGTCCCTCTACCCGCTGCTGAAAGACCCCTCCCT

1015 1016 GAATTCTTGCCCCATCTTCAGACCTGGGTGCATAACATCACCCGAGGCAAGGGCATGGGT 1075 1129 .130 CGCTGGTCTTTGCCCTATGAAAGGTTTCTCGACTTCAGAAAGCCTGTGGCGATGCCATG 1189 1190 AATTTGCTGGGCTACGCCACGTCAGATCTGAACAGAAACAGAAACCTGTTGCTGGAT 1249 294 314 334 901 274 217 ProIleLeuAlaArgAspAsnGlyIleValLeuGlyThrAsn---GlyLySTrpValGlu | | | | ::: | | | ::: | | | ::: | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | | ::: | | | | | ::: | | | | | ::: | | | | | ::: | | | | | ::: | | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | | ::: | | | ::: | | | ::: | | | ::: | | | ::: | | | ::: | | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | | ::: | :: | :: | | ::: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: 902 -----ACCATCCAGTCCTTGCCCAAGGCCCTGCAGGAACGCTACCTGCTTGTGCGCTAT |||::::: 256 AlaAlaThrLeuLysPro---ProProPheLeuArgGlyArgTyrArgLeuValArgPhe 782 GGAGATCTCATGATTGACAGTCGCATTGTGATGGGGCAGCATGAGCAAAAACTCAAGAAG 842 GAGGACCAACCTACTATGTGATGCAGGTCATCTGCCAAAGCCAGCTGGAGATCTACAAG 956 GAGGACCTGGCTCGAGCCCCTGTGGCCCAGACTTCCCGAATGTATGAATTCGTGGGATTG CTTCTG------CTCTACCTGGACTGCTGAG 1276 ||||:: |LeuvalLeuproArgGlyProAspHisPheSerTrpAlaSerProAsp 1250 375 8 8 8 ठ व ठ 요 상 요 à ద a 8 6 ò g & à

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.	OM nucleic - protein search, using frame_plus_n2p model .	Run on: May 6, 2004, 11:05:49; Search time 93.5 Seconds (without alignments) 12129.816 Million cell updates/sec	Title: US-09-645-078-1 Perfect score: 3742 Sequence: 1 gaattccattgtgttgggtatgggatcctaaaaaaaaa 2043	Scoring table: BLOSUM62 Kgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 7.0 Fgapop 6.0 , Fgapoxt 7.0 Deloop 6.0 , Delext 7.0	1140673 seqs, 277566755 residues	Total number of hits satisfying chosen parameters: 2281346 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries	Command line parameters: -MODEL=frame+ n2p.model -DEV=x1p -Q=/cgn2_1/USPTO_spool_p/US09645078/runat_06052004_104601_21872/app_query.fasta_1.2183	-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100	7 01	-LONGICG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 Database : Published Applications AA:*	400	4: /cgnz_6/ptodata/1/pubpaa/USO6_PUBCOMS.pep; * 5: /cgnz_6/ptodata/1/pubpaa/USO7_NEW PUB.pep; * 6: /cgnz_6/ptodata/1/pubpaa/USO8_NEW PUB.pep; * 7: /cgnz_6/ptodata/1/pubpaa/USO8_NEW PUB.pep; * 8: /cgnz_6/ptodata/1/pubpaa/USO8_PUBCOMS.pep; * 9: /cgnz_6/ptodata/1/pubpaa/USO9A_PUBCOMS.pep; *	10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:* 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:* 12: /cgn2_6/ptodata/1/pubpaa/US09_NBW_PUB.pep:* 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*	<pre>14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:* 15: /cgn2_6/ptodata/1/pubpaa/US10_RW PUB.pep:* 16: /cgn2_6/ptodata/1/pubpaa/US10_RW PUB.pep:* 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW PUB.pep:* 18: /cgn2_6/ptodata/1/pubpaa/US60_NEW PUB.pep:*</pre>	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		kesult. No. Score Match Length DB ID

	US-10-007-262-1 Sequence 1, Application US/10007262 Sequence 1, Application US/10007262 Publication No. US20020164748A1 GENERAL INFORMATION: APPLICANT: Bistrup, Annette APPLICANT: Rosen, Steven D. APPLICANT: Tangemenn, Kirsten TITLE OF INVENTION: GINCOSYL SULFOTRANSFERASE-3 FILE REFERENCE: 6510-107CIP CURRENT APPLICATION NUMBER: US/10/007,262 CURRENT FILING DATE: 2001-11-08 PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/190,911 PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-12 NUMBER: OF SEQ ID NOS: NUMBER: OF SEQ ID NO	SEQ ID NO 1	Qy 128 ATGCTACTGCCTAAAAAATGAAGCTCCTGCTGTTTCTGGTTTCCCAGATGGCCATCTTG 187 Db 1 MetLeuleuProLysLeuleuleuPheleuValSerGlnMetAlaileLeu 20 Db 188 GCTCTATTCTCCACATGACACCACACACACTGTTATAAAGCACAGCCC 247 Db 21 AlaLeuPhePheHisMetTyTCSTCATAAAACCACACACACACACACACACACACACACA	Oy 308 CTTTTGGGCAGCACCAGATGTTTCTACCTGATGGAGCCGCCTGGCATGTGGATG 367
Score	Qy 248 GAGCGATGCACGTGCTGTTTTCTGTCTTTTTGTGGGGCAG 307 Db 41 GluArgMetHisValLeuValLeuValLeuSerSerTrpArgSerG1ySerSerPheValG1yGln 60 Qy 308 CTTTTTGGGCAGCACCCAGATGTTTTCTACCTGATGGAGCCGCCTGGCATGGATG 367 Db 61 LeuPheG1yG1nHisProAspValPheTyTLeuMetG1uProAlaTrpHisValTrpMet 80 Qy 368 ACCTTCAAGCAGAGCACCGGATGCTTGCACAGCGGGATCTGATACGGGAC 427 Db 1	09 488 TCCAGCTCTTTCAGTGGGAGAACAGCGGGCCTGTGTTCTGCACCTGCTGACATC 547	QY 728 GTGCACCTGGTCCCGGGCCGTTCCGAGAACGCAAAGGGAGAT 787 DD 201 ValHisleuValArgAspFrOArgAlaValPheArgSerArgGluArgThrLySGlyAsp 220 QY 788 CTCATGATTGACGCATTCTGATGGGCAACGACAAAACTCAAGAAGGAGACA 647 DD 221 LeuMetII=	OY 908 CAGTCCTTGCCCAAGGCCTTGCAGGAACGTTGTTGTGCTATGAGGACCTGGTT Db 261 GlnSerLeuProLysAlaLeuGlnGluArgTyrLeuLeuValArgTyrGluAspLeuAla 280 908 CGAGCCCTGTGGCCCAGACTTCCCGAATGTATTCGTGGGATTTGGAATTCTTGCC 1027

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TCTCATGATTGACAGTCGCATTGTGATGGGGCCAGCATGAGCAAAAACTCAAGAAGGAGGA 846
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CTHER INFORMATION: Incyte ID No. US20030175923A1 2617407CD1
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PRIOR APPLICATION NUMBER: US 60/172,220
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: US 60/155,248
PRIOR APPLICATION NUMBER: US 60/133,642
PRIOR FILING DATE: 1999-05-11
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL Program
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; Publication No. US2003017592341
; Publication No. US2003017592341
; GENERAL INFORMATION:
    APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
    APPLICANT: CORLEY, Neil C.; GUBGLER, Karl
    APPLICANT: CORLEY, Neil C.; GUBGLER, Karl
    APPLICANT: ALMS, Mariah R.; LAL, Preeti G.;
    APPLICANT: AZIMZAI, Yalda
    TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
    FILE REFERENCE: PF-0552-1 DIV
    CURRENT APPLICATION NUMBER: US/10/427,631
    CURRENT APPLICATION NUMBER: US/09786,240
    PRIOR APPLICATION NUMBER: US/09786,240
    PRIOR FILING DATE: 20002-03-12
    PRIOR FILING DATE: 1999-09-09
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pLeuMetIleAspSerArgIleValMetGlyGlnHisGluGlnLysLeuLysLysGluAs 240
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25 MetArgLeuProArgPheSerSerThrValMetLeuSerLeuLeuWetValGlnThrGly
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|IleLeuValPhe----SerProAlSerArgGlnValProSer---SerProAlaGly
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                                                                                                        TCGAGCCCCTGTGGCCCAGACTTCCCCGAATGTATGAATTCGTGGGAATTCTTGCC
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                                        240 pGlnProTyrTyrValMetGlnVallleCysGlnSerGlnLeuGlulleTyrLysThrll
                                                                            260 eGlnSerLeuProLysAlaLeuGlnGluArgTyrLeuLeuValArgTyrGluAspLeuAl
                                                                                                                    280 aArgAlaProValAlaGlnThrSerArgMetTyrGluPheValGlyLeuGluPheLeuPr
                                                                CCAGTCCTTGCCCAAGGCCCTGCAGGAACGCTACCTGCTTGTGCGCTATGAGGACCTGGC
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APPLICANT: Akama, Tomoya O.
TITLE OF INVENTION: Methods of Treating Macular Corneal
TITLE OF INVENTION: Dystrophy
FILE REFERENCE: P-LJ 4852
CURRENT PELING NUMBER: US/09/927,602
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: US 09/638,211
PRIOR PELING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5.
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Mismatches:
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US-09-927-602-5
Sequence 5, Application US/09927602
Patent No. US20020061562A1
GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Mus musculus
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                   61 LeuGlyGluArgValHisValLeuValLeuSerSerTrpArgSerGlySerSerPheVal
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CURRENT APPLICATION NUMBER: US/10/258,080 CURRENT FILING DATE: 2002-10-15 PRIOR APPLICATION NUMBER: US 60/203,509
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SANJANWALA, Madhusudan
GANDHI, Ameena R.
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LAL, Preeti G.
TRIBOULEY, Catherine M.
YAO, Monique G.
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APPLICANT: POLICKY, Jennifer L.
APPLICANT: HAFALIA, April J.A.
APPLICANT: BURFORD, Neil
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ARVIZU, Chandra S.
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KHAN, Farrah A.
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                         VESCUE:

Sequence 2, Application US/09927602

Sequence 2, Application US/09927602

Sequence 2, Application US/09927602

Sequence 2, Application US/09927602

Sequence 2, Application US/092602

SERVERAL INFORMATION:

APPLICANT: PAKama, Tomoya O.

TITLE OF INVENTION: Methods of Treating Macular Corneal

TITLE OF INVENTION: Methods of Treating Methods of Treating Macular Corneal

TITLE OF INVENTION: Methods of Treating Metho
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Matches:
Conservative:
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1028.50
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                            845 GACCAACCCTACTATGTGATGCAGGTCATCTGCCAAAGCCAGGTGGAGATCTACAAG---
                                                                                                                          315 ArgArgGluAlaPheLysThrSerSerArgAsnAlaLeuAsnValSerGluAlaTrpArg
785 GATCTCATGATTGACAGTCGCATTGTGATGGGGCAGCATGAGCAAAAACTCAAGAAGGAG
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APPLICANT: GRIFFIN, Jennifer A.
APPLICANT: AU-YOUNG, Janice K.
TILE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0070 USN
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1132
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335 HisAlaLeuProPheAlaLysIleArgArgValGlnGluLeuCysAlaGlyAlaLeuGln 354
                                                                                    ---ACCATCCAGTCCTTGCCCCAAGGCCCTGCAAGGCTACCTGCTTGTGCGCTATGAG 958
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Sequence 3, Application US/09927602

Patent No. US20020061562A1

GENERAL INFORMATION:

APPLICANT: Fukuda, Michiko N.

APPLICANT: Arama, Tomoya O.

TITLE OF INVENTION: Methods of Treating Macular Corneal

TITLE OF INVENTION: Dystrophy

FILE REFERENCE: P-LJ 4852

CURRENT APPLICATION NUMBER: US/09/927,602

CURRENT APPLICATION NUMBER: US 09/638,211

PRIOR FILING DATE: 2000-08-19

PRIOR FILING DATE: 2000-08-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 395
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US-09-927-602-3
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; OTHER INFORMATION: Incyte ID No. US20040029125A1 7472777CD1
US-10-258-080-5
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Matches:
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    PRIOR FILING DATE: 2000-05-11
PRIOR APPLICATION NUMBER: US 60/202,234
PRIOR PEDING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-19
PRIOR PILING DATE: 2000-04-19
PRIOR PRIOR PRIOR DATE: 2000-04-19
PRIOR PRIOR DATE: 2000-04-19
PRIOR PRIOR DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL PROGRAM
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1028.50
65.06%
53.98%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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315 1133 335	1193 TTGCTGG 355 LeuLeuG	Qy 1253 CTG 1255 :: Db 375 Val 375	RESULT 8 US-09-927-602-4 ; Sequence 4, Application US/09927602	; Patent No. US20020061562A1 ; GENERAL INPORMATION: ; APPLICANT: FUKUda, Michiko N. ; APPLICANT: Akama, Tomoya O. ; TITLE OF INVENTION: Methods of Treating Macular Cornes	; TITLE OF INVENTION: Dystrophy; FILE REFERENCE: P-LJ 4852; CURRENT APPLICATION NUMBER: US/09/927,602; CURRENT FILING DATE: 2001-08-09	; PRIOR APPLICATION NUMBER: US 09/638,211 ; PRIOR FILING DATE: 2000-08-11 ; NUMBER OF SEQ ID NOS: 38 ; SOFTWARE: FastSEQ for Windows Version 4.0	; SEQ ID NO 4 ; TYPE: PRT ; TYPE: PRT ; ORGANISM: Homo Sapien	1.67e-73 Length:	Score: 208 Score: 1009.00 Matches: 208 Percent Similarity: 66.41% Conservative: 57 Best Local Similarity: 52.02% Mismatches: 105 Query Match: 26.96% Indels: 7	09-645-078-1 (1-2043) x US-09-927-602-4 (1-390)	Oy 122 AGCACAATGCTACTGCCTAAAAAAATGAAGCTCCTGCTGTTTC ::: :: Db 12 ThrValLeuLeuLeuAlaGlnThrThrCysLeuLeuLeuPhel	Qy 182 ATCTTGGCTCTATTCTTCCACATGTACAGCCACAACATCAGCT	Qy 242 CAGCCCGAGCGCATGCACGTGCTTCTGTTCTTCCTGGCGCT 	Qy 302 GGGCAGCTTTTGGGCAGCACCAGATGTTTCTACCTGATGG 	OY 362 TGGATGACCTTCAAGCAGAGCACCGCCTGGATGCTGCACATGC	Qy 422 CGGCCGTCTTCTGTGCGACATGACGTCTTTGATGCCTACF	Qy 482 AGACAGTCCAGCCTCTTTCAGTGGGAGAACAGCCGGGCCTG7
Percent Similarity: 67.72% Conservative: 45 Best Local Similarity: 55.91% Mismatches: 102 Query Match: 27.19% Indels: 21 DB: 9 Gaps: 6 US-09-645-078-1 (1-2043) x US-09-927-602-3 (1-395)	W	Oy 185 TIGGCICTATICTICCACATGTACAGCCACAACATCAGCTCCCTGTCTATGAAGGCACAG 244	245 CCCGAGGCATGCACGTGCTTCTTCTTCTGGCGCTCTGGTCTTTTTTGTGGGG	Db 38 Glu***ArgValHisValLeuValLeuSerSerTrpArgSerGlySerSerPheValGly 57 Qy 305 CAGCTITITGGGCAGCACCAGATGTTTCTACCTGATGGAGCCCGCTGGCACGTGTGG 364	Qy 365 AIGACCTTCAAGCAGCGCCTGGATGCTGCACATGGCTGTGCGGATCTGATACGG 424	Qy 425 GCCGTCTTCTTGTGCGACATGAGCGTCTTTGATGCCTACATGGAACCTGGTCCCCGGAGA 484 :::	OY 485 CAGTCCAGCCTCTTTCAGTGGAGAGACAGCCGGGCCCTGTGTTCTGCACCTGTGTAC 544	Qy 545 ATCATCCCACAAGATGAAATCATCCCCCGGGCTCACGGGCAGCTCCTGTGCAGTGAACAG 604	Qy 605 CCCTTTGAGGTGGAGAAGGCCTGCGCTCCTACAGCCACGTGGTGCTCAAGGAGTG 664	Qy 665 CGCTTCTTCAACCTGCAGTCCCTCTACCGCTGCTGAAAGACCCCTCCCT	ATCGTCCACTCGTCCGGGACCCCCGGGCGTGTTCCGTTCCCGAGAACGCACAAAGGGA	785 GATCTCATGATTGACAGTCGCATTGTGATGGGGCAGCATGAGCAAAAACTCAAGAAGGAG	845 34 6	902ACCATCCAGTCCTTGCCCAAGGCCCTGCAGGAAGGCTACCTGCTTGTGCGCTATGAG 95	DB 256 AIMINLEGLINGFICEFICEFICH AND STATES OF THE STATES OF SECTOR OF STATES OF ST	1019 TICTIGCCCANCITCAGACCTGGGTGCATACCCGAGGCAAGGCATGGCT	1076GACCACGCTTTCCACACAAATGCCAGGAATGCCCTTAATGTCTCCCCAGGCTTGGCGC

GGAGCCCGCCTGGCACGTG 361 |||||||||||||||||||||||||||||:tGluProAlaTrpHisVal 77 TCTGGTTTCCCAGATGGCC 181 |::::::|||::: ellelleSerArgPro--- 30 CTCCCTGTCTATGAAGGCA 241 CTCTGGCTCTTTTTGTG 301 CATGGAACCTGGTCCCCGG 481 GIGITICIGCACCIGCCIGT 541 nValSerGlnAlaTrpArg 334 |||| yProSerSerProAlaGly 37 eal 90 7 05 8

	- TI	8-603-60-81
QY 542 GACATCATCACAGAGAAGAAGATCATCCCCGGGGCTCACTGCAGGCTCCTGTGCAGTCAA 601	8 f	0 1 1 1 1 1 1 1
Db 137 SeralaPheProArgGlyThrIleSerLysGlnAspValCysLyrFhrLeuCysThrArg 156	Pr	Ailgiment scores: Pred. No.:
Qy 602 CAGCCCTTTGAGGTGGTGGAGAAGGCCTGCCGCTCCTACAGCCACGTGGTGCTCAAGGAG 661		Score: Percent Similarity: Boot 10001 Similari
Db 157 GlnProPheSerLeuAlaArgGluAlaCysArgSerTyrSerHisValLeuLysGlu 176		Dest botal similari Query Match:
Qy 662 GTGCGCTTCTCAACCTGCAGTCCCTCTACCGGCTGAAAAGACCCCTCCTCAACCTG 721	מה ל	,
Db 177 ValargPhePheAsnLeuGlnValLeuTyrFroLeuLeuSerAspProAlaLeuAsnLeu 196	SO .	-09-645-078-
QY 722 CATATIGHTGACCTGGTCGGGACCCCCGGGCCGTGTTCCGGTTCCCGAGAACGCACAAAG 781	λο 	221
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Qy 782 GGAGATCTCATGATTGACAGTCGCATTGTGATGGGGCAGCATGAGCAAAAACTCAAGAAG 841	λ̄σ 	281. CGCTC
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295 InfletinfFroGinLetGluAlaTrpleHisAsnileThfHisGlySerGlyIleGly	<i>₹</i>	581 TGCAG
	- 4 <u>d</u>	53
Db 315 LysProlleGluAlaPheHisThrSerSerArgAsnAlaArgAsnValSerGlnAlaTrp 334		ų
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Db 335 ArgHisAlaLeuProPheThrLysIleLeuArgValGlnGluValCysAlaGlyAlaLeu 354		
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/ APPLICANT: Pukuda, Michiko N.	අ _ධ	113
TITLE OF INVENTION METhods of Treating Macular Corneal	δ' -	941 CTGCT
; TILD OF INVARIANCE P-LI 4852 . TIDDENW ADDITION: P-LI 4852	q _Q	127 Leule
CURRENT FILING DATE: 2001-09/92/5012 DETICE ADDRESS: 1000-09 DETICE ADDRESS: 1000-09 DETICE ADDRESS: 1100-09/09 111	δ	1001 GAATI
FILE STATES TO STATE	<u>අ</u>	147 GluPh
; SOFTWARE: FastSEQ for Windows Version 4.0	δ·	1061 GGCAA
LENGTH: 171	q c	167 GlyLy
; ORGANISM: Homo Sapien	RE RE	RESULT 10

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TICGTGGGGATTGGAATTCTTGCCCCATCTTCAGACCTGGGTGCATAACATCACCCGA 1060
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171
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114
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                .-2043) x US-09-927-602-8 (1-171)
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|LysGlyMetGly 171
2.91e-58
821.00
60.00%
60.00%
21.94%
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1124 GCTTGGCGCTGGTCTTTGCCCTATGAAAGGTTTCTCGACTTCAGAAAGCCTGTGGCGAT 1183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTGTGCGCTATGAGGACCTGGGCTCGAGCCCCTGTGGCCCCAGACTTCCCGAATGTATGAA 1003
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1064 AAGGGCATGGGTGACCACGCTTTCCACAAATGCCAGGGATGCCCTTAATGTCTCCCAG
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| Sequence 4, Application US/10212933
| Publication No. US20030008366A1
| GENERAL INFORMATION:
| APPLICANT: Unimura, Kenji
| APPLICANT: Rannagi, Hideki
| APPLICANT: Rannagi, Reiji
| APPLICANT: Rannagi, Reiji
| APPLICANT: Rannagi, Reiji
| APPLICANT: Rannagi, Reiji
| APPLICANT: Habuchi, Osami
| APPLICANT: Waramatsu, Takashi
| TITLE OF INVENTION: DNA ENCODING THE SAME
| FILE REFERENCE: TOYAMAI. 001406
| FILE REPERENCE: TOYAMAI. 001406
| FILE REPERENCE: TOYAMAI. 001406
| PRIOR APPLICATION NUMBER: US/09/263,023
| PRIOR APPLICATION NUMBER: US/09/263,023
| PRIOR PILING DATE: 1999-03-05
| PRIOR FILING DATE: 1999-03-05
| PRIOR FILING DATE: 1999-06-24
| NUMBER: OF SEQ ID NOS: 10
| SEQ ID NO 4
| LENGTH: 484
| TVER: DATE
                                                                                GAACGCACAAAGGGAGATCTCATGATTGACAGTCGCATTGTGATG----
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216 LeuCysProAlaTyr---ArgLysGluValValGlyLeuValAspAspArgValCysLys 234
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Conservative:
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Indels:
Gaps:
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598.50
54.40%
36.81%
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Best Local Similarity:
Query Match:
DB:
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Db 416 SerGlySerSerSer] Qy 1124 GCTTGGCGCTGGTCT	456 ProMetAlavall	Db 476 LysThrLeuleu 47	RESULT 12 US-09-03-790-255 ; Sequence 255, Application U ; Patent No. US20020068288A1	; GENERAL INFORMATION: ; APPLICANT: Lodes, Michael ; APPLICANT: Wang, Tongrong ; APPLICANT: Secrist, Heath ; APPLICANT: Pools	; APPLICANT: Mondamatn, Nabod ; APPLICANT: Findirias Caro ; APPLICANT: Fan, Liqun ; TITLE OF INVENTION: COMPOS ; TITLE OF INVENTION: COMPOS	FILE OF INVENIOUS: AND D. FILE REFERENCE: 210121.512 CURRENT APPLICATION NUMBER CURRENT FILING DATE: 2001	NUMBER OF SEQ ID NOS: 440 ; SOFTWARE: FastSEQ for Wind, ; SEQ ID NO 255 ; LENGTH: 531	; TYPE: PKI ; ORGANISM: Homo sapiens US-09-833-790-255		st Local Similarity: ery Match: :	248	308		4 204	488	536 GCCTGTGACAT	UD 264 meucyskrowiatyr Oy 593TGCAGTCAACAG
Alignment Scores: 4.79e-39 Length: 484 Score: 587.50 Matches: 131 Percent Similarity: 54.40% Conservative: 67 Best Local Similarity: 35.99% Mismatches: 137 Query Match: 15.70% Indels: 29 DB:	09-645-078-1 (1-2043) x US-10-212-933-4 (1-484)	Oy 248 GAGGGCATGCAGGTTCTGTCTTCCTGGCGCTCTGGCTCTTTTTGTGGGGCAG 307 ::: ::: ::: ::::	OY 308 CITITIGGGCAGCACCCAGATGITITICTACCIGAGCCCGCCTGGCACGTGGATG 367	Qy 368 ACCTTCAAGCAGGCCCGGGTGGGATGCTGCACATGGCTGTGGGGATCTGATACGGGCC 427	QY 428 GTCTTCTTGTGCGACATGAGCGTCTTTGATGCCTACATGGAACCTGGTCCCGGAGACAG 487 :::::	OY 488 TCCAGCCTCTTTCAGTGGGAGAACAGCCGGGCCCTGTGTTCTGCACCT 535	Qy 536 GCCTGTGACATCATCCACAAGATGAAATCATCCCCCGGGCTCACTGCAGGCTCCTG 592	Oy 593TGCAGTCAACAGCCCTTTGAGGTGGTGGAGAAGGCCTGCCGCTCCTACAGCCACGTG 649 Db 236 LysCysProProGlnArgLeualaArgPheGluGluGluGlysArgLysTyrArgThrLeu 255	Qy 650 GTGCTCAAGGAGGTGCGCTTCTTCAACCTGCAGTCCCTCTACCCGCTGCTGAAAGACCCC 709	OY 710 TCCCTCAACCTGCATATCGTCCACCTGGTCCGGGACCCCGGGGCGTGTTCCGTTCCCGA 769 ::: ::: :::	OY 770 GAACGCACAAAGGGAGATCTCATGATTGACAGTCGCATTGTGATG	Qy 815	Qy 845GACCAACCCTACTATGTGATGCAGGTCATCTGCCAAAGC 883 Db 336 GlyValGlyGlyProAlaAspTyTHisAlaLeuGlyAlaMetGluValIleCysAsnSer 355	Qy 884 CAGCTGGAGATCTACAAGACCATCCAGTCCTAGCCAAGGACCTAGCAGGAACGCTACCTG 943	QY 944 CTTGTGCGCTATGAGGACCTCGGCTCGAGCCCCTGGGCCCAGACTTCCCGAATGTATGAA 1003	Qy 1004 TTCGTQGGATTGGAATTCTTGCCCATCTTCAGACCTGGGTGCATACATCACCCGAGGC 1063	Qy 1064 AAGGGATGGGTGACCACGCTTTCCACACAATGCCAGGGATGCCCTTAATGTCTCCCAG 1123

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ò	>	1124	GCTIGGCGCTGGTCTTTGCCCTATGAAAAGTTTCTCGACTTCAGAAAGCCTGTGGGCGAT 1183
Ď	Dþ	436	AlatrpargthralaLeuthrPheGlnGlnIleLysGlnValGluGluPheCysTyrGln 455
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Ω	ପୁ	4 5 6	ProMetAlaValLeuGlyTyrGluArgValAsnserrroGluGluValLysAspLeuser 4/5
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αÞ	RESULT 12 US-09-833	-790	.255
	CO CL	No. 1	, Application US/09833790 IS20020068288A1
	GENERAL APPLIC	ANT:	NRMATION: Lodes, Michael J.
	APPLIC	ANT:	Wang, Tongtong Secrist, Heather
•••	APPLIC APPLIC	ANT:	Mohamath, Raodoh Indirias, Carol Y.
	APPLIC TITLE	ANT: OF II	AND
	TITLE FILE R	OF I	GNOSIS OF LUNG
	CURREN	T AP	PLICATION NUMBER: US/09/833,790 LING DATE: 2001-04-11
	NUMBER O	ARE:	SEQ ID NOS: 440 PastSEQ for Windows Version 4.0
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·• •• Þ	ŝ	: PRT NISM: 3-790	Homo sapiens -255
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Ð	US-09-645	5-078	-1 (1-2043) x US-09-833-790-255 (1-531)
u	à	248	CAGGIGGIGGITGICTICCIGGCGCTCTGGCTCTTTTGTGGGGCGG
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J	ò	308	SCACCACAGAIGTITICTACCTGAIGGAGCCCGCCTGGCACGIGTGGAIG 3
ı	ДD	184	LeupheAsnGlnAsnProGluValPhePheLeuTyrGluProValTrpHisValTrpGln 203
J	ò	368	TGCTGCACATGGCTGTGCGGGATCTGATACGGGC
ы	q _Q	204	LysLeuTyrProGlyAspAlaValSerLeuGlnGlyAlaAlaArgAspMetLeuSerAla 223
ŭ		428	GICTICITGIGGGACATGAGGGTCTITGATGCTACATGGAACCTGGICCCCGGAGACAG 487
u	qa	224	LeutyrArgCysAspLeuSerValPheGlnLeuTyrSerProAlaGlySerGlyGlyArg 243
J	ζ	488	GGAGAACAGCCGGGCCCTG
Ц	qq	244	nLeuThrThrLeu
J	٥y	536	CTCACTGCAGGCTCCTG 59:
L)	qq	264	LeuCysProAlaTyrArgLysGluValValGlyLeuValAspAspArgValCysLys 282
J	. AC	593	TGCAGTCAACAGCCCTTTGAGGTGGTGGAGAAGGCCTGCCGCTCCTACAGCCACGTG 649

PRIOR FILING DATE: 2001-11-29	Oy 143 AAAATGAAGCTCCTGCTGTTTCTGGTTTCCCAGATGGCCATCTTGGCTCTA 193	329 377 106 126 126 1485 1485	Oy 539 TGTGACATCATC CCACAAGATGAAATCATCCCCGGGCTCACTGCAGGCTCCTGTGC 595 166 CysAspProProGlyProAlaAspLeuValLeuGluGluGlyAspCysValArgLysCys 185 Oy 596 AGTCAACAGCCTTTGAGGTGGTAGAAGCCCTTCTACAGCCACGTGGTGCTC 655 186 GlyLeuLeuAsnLeuThrValAlala
	Qy 845GACCAACCCTACTAT	1064 AAGGGCATGGGTACCACACACACACACACACACACACACA	RESULT 13 US-10-211-462-97; Application US/10211462 ; Sequence 97, Application US/10211462 ; Publication No. US20040033495A1 ; GENERAL INFORMATION: ; APPLICANT: Murray, Richard ; APPLICANT: Watson, Susan R. ; APPLICANT: Watson, Susan R. ; APPLICANT: Watson, Susan R. ; APPLICANT: Bos Biotechnology, Inc. ; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis Modulators ; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators ; TITLE OF INVENTION: Wethods of Screening for Angiogenesis Modulators ; TITLE OF INVENTION: Wethods of Screening for Angiogenesis Woulators ; TITLE OF INVENTION: Wethods of Screening for Angiogenesis Modulators ; TITLE OF INVENTION: WOWBER: US/10/211,462 ; CURRENT APPLICATION NUMBER: US 09/784,356 ; PRIOR FILING DATE: 2001-02-13 ; PRIOR FILING DATE: 2001-02-14 ; PRIOR PELICATION NUMBER: US 60/310,025 ; PRIOR PILING DATE: 2001-08-03 ; PRIOR FILING DATE: 2001-08-03 ; PRIOR FILING DATE: 2001-08-03

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                                                          RESULT 15
US-09-927-602-6
; Sequence 6, Application US/09927602
; Batent No. US20020061562A1
; GENERAL INFORMATION:
    APPLICANT: Edwida, Michiko N.
; APPLICANT: Akama, Tomoya O.
; TITLE OF INVENTION: Methods of Treating Macular Corneal
; TITLE OF INVENTION: Mystrophy
; FILE REFERENCE: P-LJ 4852
; CURRENT APPLICATION NUMBER: US/09/927,602
; CURRENT PILING DATE: 2001-08-09
; PRIOR PILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 169
; CRGANISM: Homo Sapien
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850	112	910	115	970	134	1030	154			
791 ATGATTGACAGTCGCATTGTGATGGGGCAGCATGAGCAAAACTCAAGAAGGAGGACCAA 850	106 AlaArgAspAsnGluAlaAla	851 CCCTACTATGTGATGCAGGTCATCTGCCAAAGCCAGCTGGAGATCTACAAGACCATCCAG 910		TCCTTGCCCAAGGCCCTGCAGGAACGCTACCTGCTGCGCTATGAGGACCTGGCTCGA	116 ProProProPheLeuArgGlyArgTyrArgLeuValArgPheGluAspLeuAlaArg 134	971 GCCCCTGTGGCCCAGACTTCCCGAATGTATGAATTCGTGGGAATTGGAATTCTTGCCCCAT 1030		1031 CTTCAGACCTGGGTGCATAACATCACCCGAGGCAAGGGCATGGGT 1075	LeuGlualaTrpileHisAsnileThrHisGlySerGlyProGly 169	
791	106	851	113	911	116	971	135	1031	155	
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US-09-045-284A-2
i Sequence 2 Application US/09045284A
j Patent No. 6265192
i GENERAL INFORMATION:
i APPLICANT: Bistrup, Annette
APPLICANT: Bistrup, Annette
APPLICANT: Bistrup, Annette
APPLICANT: Hemmerich, Steen D.
i APPLICANT: Bistrup, Steven D.
i APPLICANT: Bistrup, Steven D.
i TITLE OF INVENTION: GLYCOSYL
CURRENT APPLICATION UNDMER: US/09/045,284A
CURRENT APPLICATION UNDMER: US/09/045,284A
i CURRENT APPLICATION NOMBER: US/09/045,284A
i CURRENT APPLICATION NOMBER: US/09/045,284A
i CURRENT APPLICATION NOMBER: US/09/045,284A
i CURRENT PRIBOR OF SEQ ID NOS: 9
i SEQ ID NO : 9
i ENGTHARE: PASTERQ for Windows Version 4.0
i STENGTH: 386
i TYPE: PRI ORGANISM: Homo sapiens
US-09-045-284A-2
US-09-252-991A-23896
US-09-252-991A-23948
US-09-252-991A-23948
US-09-252-991A-19777
US-09-252-991A-30422
US-09-252-991A-30424
US-09-252-991A-30424
US-09-252-991A-30424
US-09-252-991A-30424
US-09-252-991A-30424
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Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-263-023-4
US-09-471-867-2
US-09-471-867-4
US-09-11-1867-4
US-09-015-188-2
US-08-655-878-2
US-08-655-878-2
US-09-252-991A-23373
US-09-252-991A-23373
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Xgapop 10.0 , Xgapext 0
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                                      Sequence 1, Application US/09190911

Patent No. 6365365

GRNERAL INFORMATION:
APPLICANT: Bistrup, Annette
APPLICANT: Rosen, Steven D.
APPLICANT: Tangemenn, Kirsten
APPLICANT: Hemmerich, Steven D.
APPLICANT: Hemmerich, Steven D.
APPLICANT: Hemmerich, Steven D.
CURRENT Hemmerich, Steven D.
FILE REFERRNCE: 6510-1070TP
CURRENT FULLNG DATE: 1998-11-12
EARLIER APPLICATION NUMBER: 09/045,284

EARLIER APPLICATION NUMBER: 09/045,284

SARIER FILING DATE: 1998-03-20
NUMBER: OF SEQ ID NOS: 8

SOFTWARE: FREUSER FOR WINDOWS Version 3.0

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Matches:
Conservative:
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; ORGANISM: H. sapiens
US-09-190-911-1
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Pred. No.: 6.29e-186 Length: 386 Score: 1984.00 Matches: 383 Percent Similarity: 99.48* Conservative: 2 Best Local Similarity: 98.97* Mismatches: 1 Query Match: 4.02* Indels: 2 DB: 4.02* MS-09-786-240-11 (1-386)	OY 128 ATGCTACTGCCTAAAAAATGAAGCTCCTGCTGTTTCTGGTTTCCCAGATGGCCATCTTG 187	Oy 188 GCTCTATTCTTCCACATGTACAGCCACAACATCAGCTCCCTGTCTATGAAGGCACAGCCC 247	Oy 248 GAGGGAIGCACGIGCTGGTTCTGTTTCCTGGCGCTCTGGCTCTTTTTTTGIGGGCAG 307 [Qy 308 CTTTTGGCCAGCACCCAGATGTTTTCTACCTGATGGACCCGCCTGGCACGTGTGGATG 367	OY 368 ACCTTCAAGCACGCCCTGGATGCTGCACATGGCTGTGCGGGATCTGATACGGGCC 427	Qy 428 GTCTTCTGTGCGACATGAGCGTCTTTGATGCCTACATGGAACCTGGTCCCCGGAGACAG 487	Qy 488 TCCAGCCTCTTCAGIGGGAGAACAGCCGGGCCCTGIGTTCTGCACCTGCCTGTGACATC 547	OY 548 ATCCCACAAAATCATCCCCCGGGCTCACTGCAGGCTCCTGTGCAGTCCACGCCC 607	OY 608 TITGAGGIG-GIGGAGAAGGCCTGCCGCTCCTACAGCCACGIGGTGCTCCAAGGAGGTGC 666	Qy 667 CTTCTTGAACCTGCAGTCCCTCTACCCGCTGCTGAAAGACCCCTCCCT	OY 727 CGTGCACCTGGACCCCGGGCCGTGTTCCGATACCGAGAACGCACAAAGGGAGA 786	Qy 787 TCTCATGATTGACAGTCGCATTGTGATGGGGCAGCACATGAGCAAAAACTCAAGAAGGAGGA 846	OY 847 CCAACCCTACTATGTGATGCAGGTCATCTGCCAAGCCAGCTGGAGATCTACAAGACCAT 906	907	967 TCGAGCCCTGTGGCCCCAGACTTCCCGAATGTATGAATTCGTGGGAATTCTTGCC 10	Db 280 aArgAlaProValAlaGlnThrSerArgMetTyrGluPheValGlyLeuGluPheLeuPr 300	OY 1027 CCATCTTCAGACCTGGGTGCATAACATCACCGGAGGCAAGGGCATGGGTGACCACGCTTT 1086	
Qy 728 GTGCACCTGGACCCCCGGGCCGTGTTCCGTTCCCGAGAACGCACAAAGGAGAT 787 Db 201 VAHISLEUVALAYAGASPFOARGATGATATATATATATATATATATATATATATATATAT	OY B48 CAACCTACTATGTGATGCAGGTCATCTGCCAAAGCCAGGAGATCTACAAGACCATC 907	Oy 908 CAGTCCTTGCCCAAGGCCCTGCAGGAACGCTACCTGCTTGTGCGCTATGAGGACCTGGCT 967	OY 968 CGAGCCCCTGTGGCCCAGACTTCCCGAATGTATGAATTCGTGGGATTGGAATTCTTGCC 1027	QY 1028 CATCTTCACACCTGGGTGCATAACATCACCCGAGGCAAQGGCATGGGTGACCACGCTTTC 1087	OY 1088 CACACAAATGCCCATAATGTCTCCCAGGCTTGGCGCTGGTCTTTGCCCTAT 1147	OY 1148 GAAAAGGITTCTCGACTTCAGAAAGCCTGTGGCGATGCCATGAATTTGCTGGGGGTACCGC 1207	OY 1208 CACGTCAGATCTGAACAAGAACAGAAACCTGTTGCTGGATCTTCTGTCTACCTGGACT 1267	Qy 1268 GTCCCTGAGCAAATCCAC 1285 	RESULT 3 US-09-786-240-11 ; Sequence 11, Application US/09786240	; Patent No. 6588935 ; GENERAL INFORMATION: ; APPLICANT: INCYTE PHARMACEUTICALS, INC. ; APPLICANT: TANG, Y. TOM	# APPLICANT: COCKLEY, Narl C. # APPLICANT: GUEGLER, Karl J. # APPLICANT: LAL, Preeti	; AFFLICANT: YUE, Henry ; APPLICANT: HILMAN, Jennifer L. ; APPLICANT: AZIMZAL, Yalda ; TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS	ed: 09/186.779: unassigned:	11-04; 1998-11-04; 1999-05-11)) ORGANISM: Homo sapiens) FEATURE:	; NAMES/AET: MISC LEGULE ; OTHER INFORMATION: Incyte ID No. 6558935 2617407CD1 US-09-786-240-11	Alignment Scores:

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Sequence 2, Application US/09471867
Patent No. 6455289
GENERAL INFORMATION:
APPLICANT: Unchimura, Hideki
APPLICANT: Muramatsu, Hideki
APPLICANT: Radomatsu, Kenji
APPLICANT: Rannaqi, Rediji
APPLICANT: Habuchi, Osami
APPLICANT: Muramatsu, Takashi
CURRENT APPLICANTON NUMBER: US/09/471,867
CURRENT FILING DATE: 1999-12-23
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                    GCCTGTGACATCATCCCACAAGATGAAATCATCCCCCGGGCTCACTGCAGGCTCCTG---
                                                                                                                        ---TGCAGTCAACAGCCCTTTGAGGTGGTGGAGAAGGCCTGCCGCTCCTACAGCCACGTG
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Sequence 2, Application US/09263023

Patent No. 6037159

GENERAL INPORMATION:

APPLICANT: With a manatesu, Hideki

APPLICANT: Maranatesu, Kenji

APPLICANT: Maranatesu, Kenji

APPLICANT: Kannagi, Reiji

APPLICANT: Kannagi, Reiji

APPLICANT: Maranatesu, Takashi

TITLE OF INVENTION: POLYPEPTIDE OF N-ACETYLGLUCOSAMINE-6-0-SULFOTRANSFERASE AND

TITLE OF INVENTION: DOLADUS

FILE REFERENCE: TOYAM41. 001AUS

TITLE OF INVENTION WUMBER: US/09/263,023

CURRENT APPLICATION NUMBER: US/09/263,023

CURRENT FILING DATE: 1998-03-05

EARLIER APPLICATION WUMBER: UP 10-54007

EARLIER PILING DATE: 1998-03-05

EARLIER PILING DATE: 1998-03-05

SERLIER FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 10

SOFTWARE: FastsEQ for Windows Version 3.0

SEQ ID NO 2.
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pacent No. 6037159

GENERAL INFORMATION:

PAPLICANT: Withmura, Kenji

APPLICANT: Mismatteu, Hideki

APPLICANT: Kadomatteu, Kenji

APPLICANT: Kadomatteu, Kenji

APPLICANT: Kadomatteu, Resiji

APPLICANT: Kannagi, Resiji

APPLICANT: Kannagi, Resiji

APPLICANT: Kannagi, Resiji

APPLICANT: Mismatanteu, Takashi

APPLICANT: Mismatanteu, Takashi

APPLICANT: Mismatanteu, Takashi

APPLICANT: Mismateu, Takashi

APPLICANT: Mismateu, Takashi

APPLICANT: Winamatteu, Takashi

APPLICANT: Winamatteu, Takashi

APPLICANT: Winmatteu, Takashi

APPLICANT: Winmatteu, Takashi

APPLICANT: Winmatteu, Takashi

APPLICANT: Windows Version 3.0

BARLIER PILING DATE: 1998-06-24

NUMBER: Patteu PaplicAnton NUMBER: JP 10-177844

BARLIER PILING DATE: 1998-06-24

NUMBER: Patteu PaplicAnton NUMBER: JP 10-177844

BARLIER PILING DATE: 1998-06-24

NUMBER: Patteu PaplicAnton NUMBER: JP 10-177844

BARLIER PAPLICANTON NUMBER: JP 10-177844
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                                                CTIGIGGCIATGAGGACCTGGCTCGAGCCCCTGTGGCCCCAGACTTCCCGAATGTATGAA
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   ; EARLIER APPLICATION NUMBER: US 09/263,023
EARLIER FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: UP 10-54007
; EARLIER FILING DATE: 1998-03-05
; EARLIER FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
                                                                                                                                                                                                                                                 6.81e-50
598.50
54.40%
36.81%
                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-471-867-2
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S-09-471-867-4 Sequence 4, Application US/09471867 Patent No. 6455289 GENERAL INFORMATION:

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APPLICANT: Kadomatsu, Kenji
APPLICANT: Kadomatsu, Kenji
APPLICANT: Kannagi, Reiji
APPLICANT: Kannagi, Reiji
APPLICANT: Habuchi, Osami
APPLICANT: Habuchi, Osami
TITLE OF INVENTION: POLYPEPTIDE OF N-ACETYLGLUCOSAMINE-6-0-SULFOTRANSFERASE AND
TITLE OF INVENTION: POLYPEPTIDE OF N-ACETYLGLUCOSAMINE-6-0-SULFOTRANSFERASE AND
TITLE OF INVENTION: DATE STATE SAME
FILE REFERENCE: TOYAMI. 001AUS
CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: US 09/263,023
EARLIER FILING DATE: 1999-03-05
EARLIER FILING DATE: 1998-03-05
EARLIER FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSQ for Windows Version 3.0
SSPTWARE: FASTSQ for Windows Version 3.0
SSPTWARE: PASTSQ for Windows Version 3.0
                                                                              AND
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Matches:
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587.50
54.40%
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Uchimura, Kenji
Muramatsu, Hideki
Kadomatsu, Kenji
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Best Local Similarity:
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CRGANISM: Homo
US-09-471-867-4
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Pred. No.:
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316 ArgAlaHisArgMetProPheLeuGluAlaAlaGlyHisLysLeuGlyAlaLysLysGlu 335
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                                   -------GGGCAGCATGAGCAAAACTCAAGAAGGAG 844
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Sequence 2, Application US/09015188C

Sequence 2, Application US/09015188C

Patent No. 6399358

Patent No. 6399358

PAPLICANT: Williams, Kevin J

APPLICANT: Tabas, Ira

TITLE OF INVENTION: 6-Sulfotransferase

FILE REPERCES JEFF-0231

CURRENT APPLICATION WUMBER: US/09/015,188C

CURRENT FILING DATE: 1998-01-29

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 17
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CORGANISM: Homo sapiens
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329	GITTICTACCTGATGGAGCCCGCTGGCACGTGTGGATGACCTTCAAG 376
377	CAGAGCACCGCCTGGATGCTGCACATGGCTGCGGGGATCTGATACGG 424
425	GCCGTCTTCTTGTGCGACATGAGCGTCTTTGATGCCTACATGGAACCTGGTCCCCGGAGA 484
485	CAGTCCAGCCTCTTTCAGTGGAAAACAGCCGGGCCCTGTGTTCTGCACTGCC 538
539	TGTGACATCATCCCACAAGATGAAATCATCCCCCGGGCTCACTGCAGGCTCCTGTGC 595
596	AGTCAACAGCCCTTTGAGGTGGTGGAGAAGGCCTGCCGCTCCTACAGCCACGTGGTGCTC 655
656	556 AAGGAGGIGGCTTCTTCAACCIGCAGTCCCTCTACCGCTGCTGAAAGACCCCTCCTC 715
716	AACCTGCATATCGTGCACCTGGTCCGGGACCCTGGGCCGTGTTCCGTTCCGGAGACGC 775
776	ACAAAGGGAGATCTCATGATTGACAGTCGCATTGTGATGGGGCAGCATGAGCAAAAGTC 835
836 263	AAGAAGGAGGACCCAACCCTACTATGTGATGCAGGTCATCTGCCAAAGC 883
884	CAGCTGGAGATCTACAAGACCATCCAGTCCTTGCCCAAGGCCCTGCAGGAACGCTACTG 943
944	CITGIGGGCTAIGAGGACCTGGCTCGAGCCCCTGTGGCCCCAGACTTCCCGAATGTAIGAA 1003
1004	TTGTGGGGATTGGAATTCTTGCCCCATCTTCAGACCTGGGGGAAACATCACCCGAGGC 1063
1064	AAGGGCATGGCTGACGCTTTCCACACAATGCCAGGGATGCCCTTAATGTCTCC 1120
1121	CAGGCTITGGCGCTGGTCTTTGCCTATGAAAGGTTTCTCGACTTCAGAAAGCCTGTGGC 1180 ::
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                                                                AAGGCCTGCCGCTCCTACAGCCACGTGCTCAAGGAGGTGCGCTTCTTCAACCTGCAG
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                                      GATGCCTACATGGAACCTGGTCCCCGGAGACAG-----TCCAGCCTCTTTCAGTGGGAG
                                                                                                                    509 AACAGCCGGGGCCCTGTGTTCTGCACCTGCCTGTGACATCCCCACAA---GATGAAATC
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US-08-899-514-2
Sequence 2, Application US/08899514
Sequence 2, Application US/08899514
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HABUCH, OSAMI
APPLICANT: HABUCH, OSAMI
TITLE OF INVENTION: POLYPEPTIDE OF GLYCOSAMINOGLYCAN
TITLE OF INVENTION: SULFOTRANSFERASE ORIGINATING FROM HUMAN AND I
TITLE OF INVENTION: FOR THE POLYPEPTIDE
NUMBER OF SEQUENCES: 9
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144 ProLeuTrpHisIleGluArgThrValThrPheGluProGlyGlyAlaAsnAlaValGly 163
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    378 GlnValLeuAlaGlnLeuGlyTyrLysIleAlaAlaSerGluGluGluLeuLysAsnPro 397
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                                                                                                                                 RESOURCE 2, Application US/08655878

Sequence 2, Application US/08655878

Sequence 2, Application US/08655878

Parent No. 582713

APPLICANT: HABUCIN, MASAKAZU

APPLICANT: HABUCIN, OSAMI

TITLE OF INVENTION: DA CODING FOR SULFOTRANSFERASE

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

STREET:
CITY:
STATE:
CONDUTER: Eloppy disk
COMPUTER: ISP Compatible
COMPUTER: ISP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,878

FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGRAT INFORMATION:
NAME:
BATTORNEY/AGRAT INFORMATION:
BATTORNEY/AGRATICALING INFORMATION:
BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORNEY/BATTORN
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Matches:
Conservative:
Mismatches:
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REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                           1241 TIGCIGGATCTTCIG 1255
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500.50
54.02%
33.24%
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 458
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-655-878-2
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Best Local Similarity:
Query Match:
DB:
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Score:
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ASCULATION OF SECTIONS

Sequence 31978, Application US/09252991A

Sequence 31978, Application US/09252991A

Sequence 31978, Application US/09252991A

Sequence 31978, Application US/09252991A

TEREPROBALINGNATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196 136

CURRENT FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142

LENGTH: 472
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                                                                                                                                                                                                                                                                                                                                                                                                                          383 ArgGluMetTyrProPheAlaGlyIleProLeuThrProGlnValGluAspTrpIleGln 402
                                                                                                                                                                                                                                                               872 ATCTGCCAAAGC---CAGCTGGAGATCTACAAGACCATCCAGTCCTTGCCCAAGGCCCTG 928
                                                                                                                                                                                                                                                                                                                                                 344 AsnCysGluSerIleArgLeuSerAlaGluLeuGlyLeuArgGln---ProAlaTrpLeu 362
                                                                                                                                                                                                                                                                                                                                                                                                    929 CAGGAACGCTACCTGCTTGTGCGCTATGAGGACCTGGCTCGAGCCCCTGTGGCCCCAGACT 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   403 LysAsnThrGlnAlaAlaHisAspGlySerGlyIleTyrSerThrGln---LysAsnSer 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 AlaProCysGlyProAlaMetArgLeuPheGlyTyrLysLeuAlaArgAspAlaAlaAla 461
          TCCCTCAACCTGCATATCGTGCACCTGGTCCGGGACCCCCGGGGCCGTGTTCCGTTCCCGA 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1169 AAAGCCTGTGGGGGATGCCATGAATTTGCTGGGCTACCGCCACGTCAGATCTGAACAAGAA
                                                                                                                                                       770 -----GAACGCACAAAAGGGAGATCTCATGATTGACAGTCGCATTGTG
                                                                                                                                                                                                                                       812 ATGGGGCAGCATGAGCAAAAACTCAAGAAGGAGGACCAACCCTACTATGTGATGCAGGTC
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Indels:
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462 LeuThrAsnArgSerValSerLeuLeu 470
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US-09-252-991A-31978
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         479 CGGAGACAGTCCAGCCTCTTTCAGTGGGAG-----AACAGCCGGGCCCTGTGTGTTCTGCA 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 GluhspHisLeuThrGlnPheMetPheArgArgGlySerSerArgSerLeuCysGluAsp 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBEE, MARTENS, OLSON & BEAR, LLP
STREET: 620 NEWPORT CENTER DRIVE, SIXTEENTH FLOOR
CITY: NEWPORT BEACH
STATE: CALIFORNIA
CONTRY: US
ZIP: 92660
COMPUTER REPABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
COMPUTER: DatentIn
COMPUTER: DatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,514
FLILIG DATE:
FLILIG DATE:
FLILIG DATE:
FLILIG DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DANIEL B ALTWAN
REGISTRATION NUMBER: TOYAM21.001AUS
TELEPHONE: 714 760 9502
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENDRANE CHARACTERISTICS:
LENDRANE CHARACTERISTICS:
LENDRANE CHARACTERISTICS:
LENDRANE CHARACTERISTICS:
LENDRANE CHARACTERISTICS:
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Matches:
Conservative:
Mismatches:
Indels:
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482.00
52.72%
32.38%
12.88%
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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102 AGANTTCCATCCACCAMTATCCCCACTCTCGGG	8 8		227 393 Pr
89	3 &	CGAATTCATACATTCGGGAAGTCTGGG	170
105 Prodlyhlahala	음 장	SerProHisProProGlyValProGlyArgThrAlaAspAlaThr CAGGGGCTCGAGGTCCTCATAGCGCACAAGCAGGTAGCGTT	110
155 This control of the control	QQ	ProGlyAlaAlaProGluSerValThrValArgAlaH1sArgGluSerAlaSerAlaGly	423
145 Alaskargicongorgogeneracente and analysis and a test to the analysi	à á		443
145 Alakladrg	g &		38 CCCTTCTGT 30
15 TUTGAGTTTTGGTCATGCTCCCCATCACAATGCGACTCTCAAACACCCCACACAATGCGACTCTCAATTCTCCCATCACAATGCCAATCCACATCTCCCCAAACCCACAACCCACACCCACACCCACACCAC	qq	AlaalaargProAlaAlaalabeuArgGlnProAlaProHisSerGlyGlySerProPro	463 ProMetCys 46
165 ThrserAlaieabarghis	40	TCTTGAGTTTTTGCTCGATGCCCCATCACAATGCGACTGTCAATGAGATCTCCCT	RESULT 12 US-09-12-2 1 Sequence 23373, Application US/09252991A
1777 Given	<u>අ</u> දි	ArgArgValArgCysPro	; Patent No. 6551795 ; GENERAL INFORMATION: APDIJCANT: MAYC J. Rubenfield et al.
	3 A	GlyAlaAlaGlyAsnGlyArgArgAlaAlaArgFroGlyArgFroGlyGluSerFro	TITLE OF INVENTION: NUCLEIC ACID AND A
197 LeualadiydinGluargàladiyvalvalalaprohlavaldinTrphlaroprohla 216 PRIOR APPLIES 197 LeualadiydinGluargàladiyvalvalalaprohlavaldinTrphlaroprohladis 216 PRIOR APPLIES PRIOR APPLIES PRIOR FILIN PRIOR	ò	CCAGGTGCACGATATGCAGGTTGAGGGAGGGGTCTTTCAGCAGGGGGTAGAGGG	FILE REFERENCE: 107196.136; (CURRENT APPLICATION NUMBER: US/09/252,9
683 ACTOCAGGTGAAGGGCACCTCTGAGCCCCAAGGCGCAGG	qq	a 21	CURKENI FILING DAILS: 1999-02-18 FIRST APPLICATION NUMBER: US 60/074,76 PRIOR PILING DATE: 1998-02-19
	ठे द	1 8	PRIOR APPLICATION NUMBER: US 60/094,19 PRIOR FILING DATE: 1998-07-27 FILING TO THE TO THE TOTAL
TYPE: PRT	3 8	gg g	, SEQ ID NO 23373 , LENGTH: 618
587 GCCTGCAGTGAGCCGGGGGATGATTTCATCTTGTGGATGATGTCACAGGCAGG	qq	:::	/ TYPE: PRT / ORGANIS Peudomonas aeruginosa
247	ò	GCCTGCAGTGAGCCCGGGGGATGATTTCATCTTGTGGGATGATGTCACAGGCAGG	SOTOS
527 AACACAGGCCCGGCTGTTCTCCCACTGAAAGAGCTGGCTCGCGGACCAGGTT 468 523 ArgSerThrProGlyAlaProAlaAlaHisProGlyGluProProAlaAlaProProIle 272 523 ArgSerThrProGlyAlaProAlaAlaHisProGlyGluProProAlaAlaProProIle 272 67CCATGTAGGCAT	qq	CysArgArgThrValArg	8.82e-08
253 ArgSerThrProdiyAlaProAlaAlaHisProdiyGluProProAlaAlaProProlie 272 467	δλ	IGTICICCCACTGAAAGAGGCTGACTGTCTCCGGGGACCAGGTT	in Similarity: 32.88% Local Similarity: 26.03%
467	QQ	AlaProAlaAlaHisProdlyGluProProAlaAlaProProile	/ Match: 4.59%
273 ArgProdlyProValArgArgValProAlaSerAspArgArgAla 292 443 TGTCGC	λŏ)-645-078-1 (1-2043) x US-09-252-99
293 IleArgArgThrProAladlySerValArgArgFroProAlaLySeArgArgArgArgArgArgArgArgArgArgArgArgArgA	8 8		1585
404CCATGTGCAGCA	7 A		158
313 ProAlaFIN	ò	38	1525
383 TGCTCTGCTTGAAGGCGCGCGCGCCCCATCAGGT 327 333 AlaThralaAlaAlaAspSerArgLeuAlaArgAlaProAlaGlyArgArgArgHis 352 326 CTGGGTGCTGCCCAAAAAGCTGCCCACAAAAGAAGCCAGAGCGCC 279 Db 186 1447 Db 1447	Op	 	166 Asple
333 AlaThrAlaAlaAlaAspSerArgLeuAlaArgAlaFirAliGlyArgArgArgArgHis 352 326 CTGGGTGCTGCCCAAAAAAGAAGAGGCCAGCAGCCCC	ζ	E	186 Glubb
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0y 278 AGGAAGACAGCACCAGCACGTGCATGCGCCCCCCCCCCC
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	250 QY 346 1218 Db 565 280	1169	1122 319	1085 339	1025 350	965 3 <i>6</i> 7	908	848 Alignment Scores Pred. No.:	806 412 712	746 US-09-645-078-	710 Qy 1037 TCTGA 710 Db 3 AlaG1 438		5 53	4/5 Qy 911 536	63 AlabeulleArgerodiyarg BArgP 485 Qy 881 TTTGGCAGATGACCTGCATCA	503 Db 81 505	Qy 821 GCTGCCCATCACAATGCGAC 3CTCAT 443 Db 81	rgThra 525 Qy 761 GGAACACGGCCCGGGGGTCCCC
220 g-LeuLeuleuleukrgGlnCysGlyGluGlykrgLeuklakspHiskrgArgAlaGlyGlyG 1327 AGGCTGACAGGTGGCAGCAAAGCCTTCTCAACCCTCTTAGTGGATTTGCTCAGGGAC	240 luGlyArgSerArgIhrHisArgThrAlaLeuGlyGinPheProGiyAlaIhrAlaGLYA 1267 AGTCCAGGTAGACAAGATCCAGCAACAGGTTTCTCTGTTCTTGTTCAG-	eralaalagluargdlydlyalaargasperoargdluhisproleupr	1168 CTGAAGTCGAGAAACCTTTTCATAGGGCAAAGACCAGGGCCAAGCCT	1121GGGAGACATTAAGGCATCCTGGCATTTGTGTGTGGAA	1084 AGCGIGGICACCCAIGCCCTIGCCTCGGGTGAIGITAIGCACCCAGGICTGAAGAIGGGG 	1024 CAAGAATTCCAATCCCACGAATTCATACATTCGGGAAGTCTGGGCCACAGGGGCTCGAGC	964 CAGGICCICATAGCGCACAAGCAGGIAGCGTICCTGCAGGGCCTIGGCAAGAACTG	907 GATGGTCTTGTAGATCTCCAGCTGGCTTTGGCAGATGACCTGCATCACATAGTAGGGGTTG	847 GTCCTCCTTCTTGAGTTTTTGCTCATGCTGCCCCATCACAAT	805 GCGACTGICAAICATGAGAICTCCCTIIGGGGITCTCGGGGAACGGAAC	ACCAGGIGCACGATAIGCAGGT	709 GGGGTCTTTCAGCAGCGGGTAGAGGACTGCAGGTTGAAGAAGCGCACCTCCTTGAGCAC	649 CACGIGGCTGTAGGAGGGGCGCCTTCTCCCACCACCTCAAAGGCTGTTGACT	458 rgProProAlaHisArgGlyArgProArgGlnSerArgAlaAspGlnArgFro 595 GCACAGGAGCCTGCAGTGAGCCCGGGGGATGATTTCATCTTGTGGGATGATGTCACAGGC	476HisHisProHisGlyLeuAspHisArgh	535 AGGTGCAGAACACAGGGCCCGGCTGTTCTCCCA [502 CTGAAAGAGGCTGGACTGTCTCGGGGACCAGGTTCCATGTAGGCGTTCAAAGACGCTCAT	505 lyaspårgglyargProvalaspglyGlyGlnProalaaladlyAspGluårgårgThra 442 GTCGCACAAGAAGACGGCCCGTATCAGATCCCGCACAGCCATGTGCAGCAT
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t al. De and amino acid sequences relating to pseudomonas for diagnostics and therapeutics TGGGCCACAGGGGTCGAGCCAGTCCTCATAGCGCACAA 945
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aGlyProArgGluLeuGlnGluGlyGlnHisProProGly 42 GALAVAIGJYAJAGITCTIGTAGATCTCCAGCTGGC 882 ACATAGTAGGGTTGGTCCTCCTTCTTGAGTTTTTGCTCAT 822 CTGTCAATCATGAGATCTCCCTTTGTGCGTTCTCGGGAAC 762 TCCAATCCCA----- CGAATTCAT------ 999 |||:::||| uProLeuProGlnProArgArgLeuHisProGlnGlyAla 22 CGGACCAGGTGCACATATGCAGGTTCAGGGAGGGGTCTT 702 TIGGGTGCTGCCCAAAAGCTGCCCCACAAAAGAAGAGCC 287 ||| :::||| |AspargargalaalabroLeuSerArgProLeuHisGln 62 || :: ||| ||||| stansperoleualaalaa 545 GGTCATCCACGTGCCAGGCGG-------G 347 :: InCysProArgAlaArgArgGluSerSerAlaAlaA 565 265 91 24 95 155 52-991A-32896 (1-265) Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: CAGCACGT 258 ||||||||| roAlaArg 583 9/252,991A /074,788 1/094,190 252991A ď

	Qy 798 ACAGTCGCATTGTGATGGGCAGCATGAGCAAAAACTCAAGAAGGAGGACCAACCTACT 857
0.00	; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-23948 Alignment Scores:

::: 127	1180 GCCACAGGCTTTCTGAAGTCGAGAAACCTTTTCATAGGGCAAAGACCAGCGGCCAAGCCTG 1121	recerrece Leu	TCGGGTGATGTTATGCACCCAGGTCTGAAGATGGGGCAAGAATTCCAATC TCGGGTGATGTTATGCACCCAGGTCTGAAGATGGGGCAAGAATTCCAATC	1010	985 CTGGGCCACAGGGGCTCGAGCCAGGTCCTCATAGCGCACAAG 944	943 CAGGTAGCGTTCCTGCAGGCCTTGGGCAAGGACTGGATGGTCTTGTAGATCTCCAGCTG 884		AIGCIGCCCAAIGCGACIGICAACAIGAGATCTCCCTTTGIGGGAAACAIGAGAAACAIGAAACAIGAAACAIGAAACAIGAAACAIGAAACAIGAAAACAIGAAAACAIGAAAAAAAA	744 763 ACGGAACACGGCCCGGGGGT744	3 69 1	COGGTAGAGGACTGCAGGTTGAAGAAGGGCACCTCCTTGAGCACCACGTGGCTGTAGGA	を こうしょ かんけい はい	GCGGCAGCCIICLCCACCACCACCACCACCACCACCACCACCACGCIGIIGACIGCACACGCACCACCACCACCACCACCACCACCACCACCAC	conditional and a control of the con	TGCAGAACACAGGGCCCGGCTGTTCTCCCACTGAAAvadGGCTGGACTG 48 1	484 TCTCCGGGGACCAGGTTCCATGTAGGCATCAAAGACGCTCATGTCGCACAAGAAGACGGC 425 	424 CCGTATCAGATCCCGCACAGGCCATGCAGGCGCTCCAGGGCGTGCTTGAAGGTCAT 365	364 CCACACGTGCCAGGCGGGCTCCATCAGGTAGAAAACATCTGGGTGCTGCCCAAAAAGCTG 305	304 CCCCACAAAAAAAGCCAGAAGACGCAGAAGAACCAGCACGTGCATGCGCTCGG 246
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Qy 858 ATGTGATGCAGGTCATCTGCCAAAGCCAGCTGGAGATCTACAAGACCATCCAGTCCTTGC 917	918 CCAAGGCCCTGCAACGCTACCTGCTTGTGCGCTATGAGGACCTGGCTCCTG	978 IGGCCCAGACTTCCCGAATGTATGAGTTCGTGGGATTGGAATTCTTGCCCATC	1032 TTCAGACCTGGGTGCATAACATCACC 1058 326TrpSerCysArgHrberPro 332	RESULT 15 US-09-252-991A-28921		; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS; FILE REFERENCE: 107196.136; CURRENT APPLICATION NUMBER: US/08/252.991A	CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR PILING DATE: 1998-02-18	FILING DATE: 1998-07-27 NUMBER OF SEQ 1D NOS: 33142 SEQ 1D NO 28921 LENGTH: 1034	; TYPE: PRT ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-28921	7.9e-07 Length: 16.50 Matches: 31.94% Conservative.		US-09-645-078-1 (1-2043) x US-09-252-991A-28921 (1-1034)	QY 1588 AGGCCTCCAGGCCACAAGTCTCTGAAGTCTGCCCAGACAGGAAGAACAAGAAAGA	Qy 1528 AGAGCAATACCCTGTTTCACTGGTGGGATGTGCTGCTCACATAAGGTT 1481	OY 1480 CCCCAGTCTGTTTTCTAGACACAAGGACACAAAAGTCCTTCTGCTTGAGCACGTGT 1421	CAGTGTGA	1360 GCAAGGCTCAGAAGCATTCAGAGAAAGTGACTGAGGCTGACACGGGGGGGCAGGCA	1300 TICTCAACCCTCTTAGTGGATTTGCTCAGGGACAGTCCAGGTAGAAGAACAACCAGCAA	DD IID IG 120 QY 1240 CAGGTTTCTCTGTTCTTGAGATCTGACGTGGCGGTAGCCCAGCAAATTCATGGCATC 1181

418 laGlyArgArgArgArgGluAspArgArgSerThrArgProSerAlaAlaAlaAlaGln 437

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Search completed: May 6, 2004, 11:08:13 Job time : 42 secs

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May 6, 2004, 10:47:57 ; Search time 20 Seconds (without alignments) 1856.496 Million cell updates/sec
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Description		N-acetylglucosamin	N-acetylglucosamin	N-acetylglucosamin	chondroitin 6-sulf	probable enzyme, C	hypothetical prote	surfactin syntheta	mei-41 protein - f	hypothetical prote	hydroxysteroid sul	resistance protein	Ħ		probable cytochrom	polyketide synthas	mitochondrial proc	probable transcrip	genome polyprotein	hypothetical prote	aminopeptidase BH3	tyrosylprotein sul	probable spectrin	hypothetical prote	protein F57B9.2 [i	methylmalonyl-CoA	ted DNZ	splicing factor PR		probable protein k
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RESULT

probable protein k	>	hypothetical prote	probable DNA recom	hypothetical prote	alpha-A-crystallin	C1 protein - Misca	threonine-tRNA lig	hypothetical prote	probable membrane	group 2 sigma 70-t	guanine nucleotide	hypothetical prote	probable phosphati	hypothetical prote
A96558	83928 S14113	T18692	T34899	T37529	149477	JQ1358	G86863	T43458	S45734	AB2337	T42726	T00270	T14176	E84536
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	855.5 5.5	85	82	82	82	84.5	84.5	84.5	84.5	84	84	84	84	83.5
30	3 F	33	34	35	36	37	38	6£.	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 JC7350 C) Acceptes: Mus musc C, Date: 08-Sep-2000 C, Date: 08-Sep-2000 C, Accession: JC7350 R, Uchimura, K.; Fas Biochem. Biophys. R A;Title: Diversity A, Reference number: A, Accession: JC7350 A, Residues: 1-484 A, Cross-references: C, Comment: This enz sulfate linkage fo C, Keywords: glycoly	RESULT 1 JC7350 JCA-cestylglucosamine-6-O-sulfotransferase (EC 2.8.2) [validated] - mouse C.Species: Mus musculus (house mouse) C.Species: JCA-cession: JC7350 R.Johnmara, K.; Rasakhany, F.; Kadomatsu, K.; Matsukawa, T.; Yamakawa, T.; Kurosawa, N. Biochem. Biophys. Res. Commun. 274, 291-296, 2000 A.Attile: Diversity of N-acerylglucosamine-6-O-sulfotransferases: Molecular cloning of a A.Accession: JC7350 A.Ac
Query Mato Best Local Matches	Query Match Best Local Similarity 34.2%; Pred. No. 1.5e-45; Matches 136; Conservative 65; Mismatches 151; Indels 46; Gaps 7;
<i>₹</i> 8	30 NISSLSMKAQPERMHVLVLSSWRSGSSFVGQLFGQHPDVFYLMEPAWHVWMTFKQSTAWM 89
6y 59	90 IAMAVRDLIRAVFLCDMSVFDAYMEPGPRRQSSIFQWBNSRALCSAPACD 139
Oy 1,	140 IIPQDBIIPRAHCRLLCSQQPFEVVEXACRSYSHVVLKEVRFFNLQSLYPLIKDPS 195
Oy 15	196 LNLHIVHLVRDPRAVFRSRERTKGDLMIDSRIVWGQHE, 233
2. 2. 2. Db 33.	234 QKLKKEDQPYYVMQVICQSQLEIYKTIQSLPKALQERYLLVRYEDLARAPVAQTSR 289
Oy 28	290 MYEFVGLEFLPHLQTWVHNITRGKGMG-DHAFHTNARDALMVSQAWRWSLPYEKVSRLQK 348 :
Oy 3.	349 ACGDAMNLLGYRHVRSEQEQRNLLLDLLSTWTV 381

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C)Accession: A57397
R)Fukuta, M.; Uchimura, K.; Nakashima, K.; Kato, M.; Kimata, K.; Shinomura, T.; Habuchi, L. Biol. Chem. 270, 18575-18590, 1995
A;Title: Molecular cloning and expression of chick chondrocyte chondroitin 6-sulfotransf A;Reference number: A57397; MUID:95355490; PMID:7629189
A;Accession: A57397
A;Accession: A57397
A;Accession: A57397
A;Accession: A57397
A;Accession: A57397
A;Crosser-references: GB:D49915; NID:g971262; FIDN:BAA08655.1; PID:g971263
C;Superfamily: chondroitin 6-sulfotransferase
C;Keywords: sulfotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPRAVLVSR------MV---APSGKYESWKKWAAEGEAPLQEDE-VQRLRGNCESIRLS 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDHAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMNLLGYRHVRSEQEQRNLLLDL 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Gallus gallus (chicken)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AELGLRQ-PRWLRGRYMLVRYEDVARAPLRKALEMYRFAGIHPTPQVEEWIRANTQAP-Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 MAV--RDLIRAVFLCDMSVFDAYMEPGPRRQ--SSLFQWENSRALCSAPACDIIPQ-DEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 FEKYHCKNRRCGPLNITLAARACRRKQHVALKTVRIRQLEFLQPLAEDPRLDLRIIQLVR
                           236 KCPPQRLARFEEECRKYRTLVIKGVRVFDVAVLAPLLRDPALDLKVIHLVRDPRAVASSR
                                                                                                                                                                                                                                                                                              356 MAKTLOTALQPPDWLQGHYLVVRYEDLVGEPVKTLRRVYDFVGLLVSPEMEQFALNMTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                          313 KGMGDHAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMNLLGYRHVRSEQEQRNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 SGSSKRFYVVSARNATQAANAMRTALTFQQIKQVEEFCYQPMAVLGYERVNSPEEVKDLS
    ERMHVLVLSSWRSGSSFVGQLFGQHPDVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRA
                                                                                                                                                                          156 -CSQQPFEVVEXACRSYSHVVLXEVRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSR
                                                                                                                                                                                                                                                                ERTKGDLMIDSRIVM-----VMQVICQS
                                                                                                                                                                                                                                                                                                                                                      253 QLEIYKTIQSLPKALQERYLLVRYEDLARAPVAQTSRMYEFVGLEFLPHLQTWVHNITRG
                                                                                      VFLCDMSVFDAYMEPGPRRQS----SLFQWENSRALCSAPACDIIPQDEIIPRAHCRLL-
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N-acetylglucosamine-6-O-sulfotransferase (BC 2.8.2.-) [validated] - human cispecies: Homo sapiens (man) cispecies: Maganana, r.; Matsukawa, T.; Yamakawa, T.; Kurosawa, N.; Biochem. Biochem. Biochem. 274, 291-296, 2000 A; Title: Diversity of N-acetylglucosamine-6-O-sulfotransferases: Molecular cloning of a A; Reference number: JC7350; MUID:20374462; PMID:1091333 A; Residues: 1486 ciUCH. A; Residues: 1486 ciUCH. A; Residues: 1486 ciUCH. A; Residues: 1286 ciUCH. A; Residues: Taks enzyme, having a type II transmembrane topology and N-linked glycosylatic; comment: This enzyme, having a type II transmembrane topology and N-linked glycosylatics sulfate linkage formation. This enzyme is involved in synthesis of L-selectin ligand in C; Keywords: glycolysis; sulfate transport; sulfotransferase; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLQTWVHNITRGKGMG-DHAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMNLLGY 359
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Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-acetylglucosamine-6-O-sulfotransferase (EC 2.8.2.-) - human C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_chang
C;Accession: JBO261
R;Uchimura, K.; Muramatsu, H.; Kaname, T.; Ogawa, H.; Yamakawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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A;Title: Human N-Acetylglucosamine-6-O-sulfotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Reference number: JB0261; MUID:98391845; PMID:9722682
A, Accession: JB0261
A, Molecule type: mRNA
A, Residues: 1-484 «UCH>
A, Cross-references: DDBJ:AB014679
C, Comment: This protein catalyzes the transfer of sulfer C; Superfamily: chondroitin 6-sulfotransferase
C; Keywords: sulfotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.9%; Score 588.5; DB 2;
llarity 36.0%; Pred. No. 1.4e-42;
Conservative 67; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                      29.8%; Score 606.5; DB 2; 37.0%; Pred. No. 3.9e-44; iive 56; Mismatches 133;
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Astronoment I - Bacillus subtilis

NiAlternate names: component I - Bacillus subtilis
NiAlternate names: competence protein srfAA; surfactin production protein srfAA; surfact
C;Species Bacillus subtilis
C;Date: 12-Aug-1996 #sequence revision 12-Aug-1996 #text_change 03-Nov-2000
C;Accession: 140485; B65718; S35517, A37323; S46967; A43705; S34985
R;Commina, P.; Rodriguez, F.; de Ferra, F.; Grandi, G.; Perego, M.; Venema, G.; van Sink
Mol. Microbiol. 8, 821-831, 1993
A;Title: Sequence and analysis of the genetic locus responsible for surfactin synthesis
A;Reference number: 140485; MUID:93360813; PMID:835569
A;Accession: 140485
A;Accession: 140485
A;Accession: 140485
A;Residues: 1-Sas «RES.
A;Cross-references: Errain W168 derivative of JH642
B;Kunst, F.; Oqsawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte:
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch.
A; Birlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Pabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
                                 Circlesion: 17-041-1999 #sequence_revision 17-041-1998 #text_change 22-Oct-1999 Circlesion: G7029 #s. Parkhill, U.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A; Authors: Sqares, R.; Sulston, U.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Pitle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70509; MUID:98295997; PMID:9634230 A; Remember: A70509; MUID:98295997; PMID:9634230 A; Remember: DNA A; Resence number: A70509 A; Remember: DNA A; Resence number: A70509 A; Remember: DNA A; Remember: A70509 B; A70509 B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KVLLEVFPQAKFIHIVRDPYVVY------PSTIHLHKALYRIHGLQQPTFDGLD 273
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obacterium tuberculosis
-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOTWVHNITRGKGMGDHA-PHTNARDALNVSQAWRWSLPYEKVSRLOKACGDAMNLLGY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 116; DB 2; Length 388;
19.3%; Pred. No. 0.037;
tive 67; Mismatches 111; Indels 1:
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IFIVGHWRTGTTLLHELLVVDDRHTGPTGYECLAP--HHFLL----TEW-
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Best Local Similarity
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RH 375
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A;Gene: Rv2267c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
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  389 DSNGIYSTQKNSSEQFEKMRFSIPPKLAQVVQDACEPAMRLFGYKLASSAQELINKSLSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 AVRDLIRAVFLCDMSVFDAYMEPGPRRQSSLFQWENSRALCSAPACDIIPQDEIIPRAHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 RLLCSQQPFEVVEKACR-----SYSHVVLKEVRFFN-LQS-------
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8.2%; Score 168; DB 2; Length 307
Best Local Similarity 22.7%; Pred. No. 9.2e-07;
Matches 83; Conservative 50; Mismatches 131; Indels
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hypothetical protein Rv2267c
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H37RV)

(strain

tuberculosis

- Mycobacterium

267 L--QERYLLVRYEDLARAPV 284

209 AVFRSRERTKGDLMID--SRIVMGQHEQKLKKEDQPYYVMQVICQSQLEIYKTIQSLPKA 266

74 PAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQSSLFQWENSRALC 133

990 VEKAGIFDNFFETGGHSLKAMTLLTKIHK--

-------CDIIPQDEII------PRAHCRLLCS

134 SAPA-----

158 QOPFEVVEKACRSYSHVVLKEVRFFNLQSLYPLLKDPSL----NLHIV-----HLVRDPR 208

q ₀		ò	Db 1	ò	Db .	λ	d d	ò	d d	δ	qa	RESULT 8	mei-41 pro	C;Species: C;Date: 13 C;Accessio	R, Hari, K	A,Title:	A; kererend A; Accessio	A;Status: A;Molecule	A;Residue: A;Cross-re	C,Genetica A,Gene: me	A; Cross-re A; Introns	C; Function A; Descripi	Query Ma	Best Lo		ें ह	g	δλ	ΩÞ	δλ	qu	ò	qC	ζ	qα	λö
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galled	iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.	Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel	y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle	Sekiguchi, J.; Sekowska	Yasumoto, K.;	A.Authors: Yoshikawa, H.F.; Zumerein, B.; Yoshikawa, H.; Danchin, A. A. A.Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A.Defended and A.Defende Schools MITTLE GOARAND.	7/55055: EMILD:93045:	Aistatus: nucleic acid sequence not shown; translation not shown. A Molecule type: DNA	A; residues: 1-3588 < KLUN> A; Cross-references: GB: Z99105; GB: AL009126; NID: g2632457; PiDN: CAB12142.1; PID: g2632634	A.Experimental source: strain 168 R.Fuma, S.; Fujishima, Y.; Corbell, N.; D'Souza, C.; Nakano, M.M.; Zuber, P.; Yamane, K.	Nucleic Acids Wes. 11, 3-5-7, 1593 A./Title: Nucleotide sequence of 5, portion of srfA that contains the region required for A,Reference number: 835517; MUID:93181186; PMID:8441623	A.Accession: 835517 A.Status: nucleic acid sequence not shown; significant sequence differences	A; Oross-references: BMBL:D13262; NID:g216345; PID:g216346	A,Experimental source: strain 168 trpC2 A,Note: protein sequence not complete, the nucleotide sequence was submitted to the EMBL P.Nabern M M Marginson D Miner B Chimit I Grassman B D Salver B		A,Title: srfA is an operon required for surfactin production, competence development, an A,Reference number: A37323; MUID:91154134; PMID:1847909	A,Accession: A37323 A,Status: nucleic acid sequence not shown; not compared with conceptual translation	A;Molecule type: DNA A;Residues: 1-46,'EV',49-145,'I',147-150,'L',152,'AN',155-280,'T',282-307,'SF',310-384	A;Cross-references: GB:M5933; NID:g14366 R;Nakano, M.M.; Xia, L.; Zuber, P.	J. Bacteriol. 173, 5487-5493, 1991 A,Title: Transcription initiation region of the srfA operon, which is controlled by the	A,Reference number: A43705; MUID:91358326; PMID:1715856 A:Contents: annotation	R;Fabret, C.; Quentin, Y.; Guiseppi, A.; Busuttil, J.; Haiech, J.; Denizot, F. submitted to the EMBL Data Library, March 1993	A;Reference number: S46967 A;Accession: S46967	A; Molecule type: DNA D. Besidhes: 3249-3271 / 22 / 2271 / 22 / 2318-3451 / Y/ 3453-3483 / DR/ 3486-3487 / DAGL/ 34	1	A;sxperimental source: strain los trpcz. C;Comment: This enzyme is one of several in the multienzyme complex that synthesizes the	nce. C;Genetics:	A, Gene: srfAA, srfAl A.Note. arfaa is the first dene of the grfA operon	urfactin synthetase; acetate CoA ligase homology; acyl car	Diolic Diobynchesis, carifer process; prospucpanceumers; prospucproces: accete-Coa ligase homology ACCI.	F;9/4-1042.Lomain: acyl carifer process sacres	F:1059-1993/Domain: acetate-CoA 11gase nomology <acla> F:2011-2019/Domain: acetate-row 11gase nomology <acp2> F:2017-2019/Domain: acetate-row 11gase nomology <acp2></acp2></acp2></acla>	1,1	/Binding	Query Mauch 4.7%; Score 95; DB 2; Length 3588;	est bocal similarity 13:7%; atches 63; Conservative 4:

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1058 NYNFASPQHLPINILSDDFAVLALTSLCRGYQF--QQNTKHVDSFSL------ 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1103 ------SIQETLA---ICGIS-------PKEQKKVQLWQ------SLPA---RMRQ 1133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RMYEFVGLEFLPHLOTW-----VHNITRGKGMGDHAFHTNAR----DALNVSQAWRWSLP 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 STAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQSSLFQWENSRALCSAPACDIIPQD 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 BIIPRAHCRLLCSQQPFEVVEKAC--RSYSHVVLKEVRFP-------NLQS 186
                                                                                                                                                                                                                                                        references: EMBL:U34925; NID:g998351; PID:g998353; PIDN:AAC46881.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 SHNISS---LSMKAOPERMHVLVLSSWRSGSSFVGQLFGQHPDVFYLMEPAWHVWMTFKQ
                                                                                                                                                                                                                                                                                                                                                                                 ption: involved in cell cycle checkpoint and meiotic recombination
                                                                                                                                                                                                                                                                                                                                                                                                                    Match 4.5%; Score 92.5; DB 2; Length 2354; ocal Similarity 20.5%; Pred. No. 42; s 85; Conservative 52; Mismatches 147; Indels 131;
                                                                                                                                                                                          : preliminary; translated from GB/EMBL/DDBJ
le type: DNA
es: 1-2354 <HAR>
                                                                                                                                                                                                                                                                                                                        references: FlyBase:FBgn0004367
s: 650/3; 748/3; 2313/3
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14 VSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFVGQLFGQHPDVFYLME

Query Match Best Local Similarity 22.2%; Pred. No. 3.8; Matches 52; Conservative 32; Mismatches 79; Indels 71; Gaps 11;	OY 67 DUFYLMEPAWHYMYFRQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQSSLFQW 126	RESULT 11 \$11737 resistance protein Mx3, interferon-regulated - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-2000 C;Accession: B:1737 R;Meier, E.; Kunz, G.; Haller, O.; Arnheiter, H. R;Meier, E.; Kunz, G.; Haller, O.; Arnheiter, H. R;Meier, E.; Kunz, G.; Haller, O.; Arnheiter, H. A;Description: Unexpected activity of rat Mx proteins against a Rhabdovirus. A;Reference number: \$1735 A;Accession: \$11735 A;Accession: \$11737 A;Molecule type: mRNA A;Residues: 1-659 < EMB> A;Cross-references: EMBL:X52713; NID:g56724; PIDN:CAA36937.1; PID:g56725 C;Superfamily: dynamin-related protein VPS1	Query Match 4.5%; Score 91; DB 2; Length 659; Best Local Similarity 20.6%; Pred. No. 10; Matches 65; Conservative 50; Mismatches 104; Indels 96; Gaps 62 FGQHPDVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAVME 1 :	OY 115	Qy 201 VHLVRD-PRAVPRSRERTKGDLMIDSRIVMGQHEQKLKKEDQPYYWMQV 248 1
QY 340 YEKVSELQKACCDAMNLLGYRHVRSEQEQRNLLLDLLSTWTVPEQI 385	M -	C;Superflucs: 28/2; 50/2; 113/2; 155/3; 220/3; 290/2 C;Superfamily: Caenorhabditis elegans hypothetical protein F42G9.8 C;Superfamily: Caenorhabditis elegans hypothetical protein F42G9.8 C;Superfamily: Caenorhabditis elegans hypothetical protein F42G9.8 Cuery Match 4.5%; Score 92; DB 2; Length 359; Best Local Similarity 19.5%; Pred. No. 3.8; Matches 63; Conservative 48; Mismatches 114; Indels 98; Gaps 15; Cy 52 RSGSFVGQLFGQHPDVFYLMEPAMHVWMTFKQSTAWMLHMAVRDLIRAVELCDMS 107 Cy 63 RSGTTLMRAILDAHPDVRCGGFTMLLESFLTWQAGWRND-WNNSGITQE 143 Cy 108 VFDDAYMEPGPRRQSSLFQMENSRALCSAPACDITPQ-DEITPRAHCRLLCSQOPFEVVEK 166 Cy 1144 VFDDAVSARITEIVARKSELAPRLCNKDP172	167 ACRSYSHVVLKEVRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLM	QY 279 LARAPVAQTSRYTEFVOLEFLPHLQTWVHNITRGKGMDHAFH-TNADALNVSQAWRWS 337 Db 252 LIQKPAREILRITNFLDLPFSQQMLRHQDLIGDEVDLNDQEFSASQVKNSINTKALTSWF 311 QY 338 LPY-EKVSRLQKAGGAAMLLGY 359 Db 312 DCFSEETLRKLDDVAPFLGILGY 334	RESULT 10 JED196 JED196 JED196 JED196 JED196 JED196 JED198

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KFFKARPNDFFVCSYPKTGTTWLKALTFA-
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Best Local Similarity 19.9<sup>3</sup>
Matches 70; Conservative
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chirologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chir, C.W.; Chung, M.K.; Coun, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.R.; Li, J.H.; Li, Y.; Lin, X.; Liu, Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Tille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: B86319
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <STO>
A;Cross-references: GB:AE005172; NID:99795597; PIDN:AAF98415.1; GSPDB:GN00141
C;Superfamily: alcohol sulfotransferase
Ribult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Science 273, 1058-1073, 1956
A.Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G.A.Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G.A.Authors: Raine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G.A.Authors: Raine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, G.A.Feference number: A64300; MUID:96337999; PMID:8688087
A.Status: preliminary; mucleic acid sequence not shown; translation not shown A.Residues: 1-1847 kBUJ.
A.Cross-references: GB:U67583; GB:L77117; NID:g2826409; PIDN:AABS9433:1; PID:g1592072; T.A.Map position: REV1393176-1387633
A.Start codon: TTG
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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larity 19.0%; Pred. No. 5.9;
Conservative 50; Mismatches 132;
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                                                        ENSRALCSAPACDI ----IPODEIIPRAHCRLLCSQOPFE----VVEKACRSYSHVVLK 177
                                                                                                                        167
                                                                                                                                                                                    EVRFFNIQSLYPLLKDPSLNLHIVHLVRDPRAVFRS-----RERTKGDLMIDSRIVMGQ 231
                                                                                                                                                                                                                                                                                                                                                     206 YCQGLSAYG-PY-----LDHVLGYWKAYQANP----DQILFLKYETWRADPLPYVKRLA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 EFMGYGFTKEEEEGNVVEKVVKLCSFET-LKNLEANKGEKDR----EDRPAVYANSAYFR 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Cross-references: EMBL:Y10493; NID:g3334666; PIDN:CAA71517.1; PID:g3334667
A)Experimental source: cultivar Harosoy 63, strain Merr
C;Superfamily: human cytochrome P450 CYP2D6, cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; moi
F;303-466/Domain: cytochrome P450 homology <P45>
F;444/Binding site: heme iron (Cy8) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Contains: oxidoreductase (EC 1.-.-.)
C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jul-2000
C;Accession: T07120
R;Schopfer, C.R.; Ebel, J.
Mol. Gen. Genet: 258, 315-322, 1998
A;Title: Identification of elicitor-induced cytochrome P450s of soybean (GlyvA;Reference number: Z15931; MUID:98311068; PMID:9648734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIRKICTLELLSAKRVQSFSHIRQDENKKLIQSIHSSAGSPIDLSGKLFSLLGTTVSRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 VEYLMEPAWHVWMTEXQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQSSLFQWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------LP---IIGNLHQLALAASLPDQALQKLVRKYGPLMHLQLGBISTLVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 SS--PKMAMEMMKTHDVHFVQRPQ------LLAPQFMVYGATDIAFAPYGDYWR
                                                                                                                                                                                                                                      ---IVYIWRDPKDTFVSMWTFAHKERSQQGPVVSIEBAFDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHLOTWVHNI TRGKGMGDHAFHTNA----
--IANRSKFDVSTNPLLKRNPHEF--
                                                                                                                                                                                                                                                                                                                HEOKLKKEDOPYYVMOVICOSOLEIYKTIOSLPKALOERYLLVRYEDLARAPVAQTSRMY
                                                                                                                                                                                                                                                                                                                                                                                                                                            --LPHLQTWVHNITRGKGMGDHAFHTNARDALNVSQA---
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                                                                                                                 -----VPYIEIDPPFFPSVDVLKDBGNTLFSTHIPYDLLPESVVKSGCK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: Tu7120
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
A;Residues: 1-504 <SGH>
A;Cross-reference: ASGH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGKVGDWQNYLTPEMVARI 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----WRWSLPYEKVSRL 346
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CiSpecies: Bacillus subtilis
CiSpecies: G5-G5-G7
CiSterion: G5-G7-G7
Cisterion: G5-G7-G7
Cisterion: G5-G7-G7
Cisterion: G5-G7-G7
Cisterion: G6-G7-G7
Cisterion: G7-G7-G7
Cisterion: G7-G7
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F;293-363/Domain: acyl carrier protein homology <ACPl  
F;414-829/Domain: acycoacyl-[acyl-carrier-protein] synthase I homology <OASl>  
F;346-2732/Domain: boxoacyl-[acyl-carrier-protein] synthase I homology <OAS>  
F;3145-3320/Domain: boxoacyl-[acyl-carrier-protein] synthase I homology <OASl>  
F;3550-3942/Domain: a-oxoacyl-[acyl-carrier-protein] synthase I homology <OASl>  
F;4138-4208/Domain: acyl carrier protein homology <ACP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; nucleic acid sequence not shown; translation not shown Molecule type: DNA
Molecule type: DNA
Molecule 1,4273 «KNU»
Moss-references: GB:229113; GB:AL009126; NID:g2634090; PIDN:CAB13603.1; PID:g2634103
Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      217 TKGDLMIDSRIVMGQHE-QKLKKEDQPYYVMQVICQSQLEIYKTIQSLPKALQERYLLVR 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 YEDLARAPVAQT-SRMYE-----FVGLEFLPHLQTWVHNIT--RGKGMGDHAFHTN 323
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4.4%; Score 89.5; DB 2; Length 4273;
Best Local Similarity 22.9%; Pred. No. 1.7e+02;
Matches 48; Conservative 34; Mismatches 87; Indels 41
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MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamiln N., Holroyd S.,
Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
Ollver S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Deciphering the biology of Mycobacterium tuberculosis from the
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                                                                                                                                                    LGIAAPEPRRHVLLMATTRIGSSFVGEPFNQQGNIFYLFEPLWHIERTVIFEPGGANAVG
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MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
Melson M., Alland D., Bison W., Garpenter L., White O., Peterson J., Bodson R., Gwinn M., Haft D., Hickey B., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L. Belcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
Whole-genome comparison of Mycobacterium tuberculosis clinical and
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Corynebacterineae; Mycobacteriaceae; Mycobacterium.
        75; Mismatches 133; Indels
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10-OCT-2003 (Rel. 42, Last annotation update)
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RV2267C OR MI2329 OR MICY339,43 OR MB2290C.
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Nature 393:537-544(1998).
        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167
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SPECIES-M. Dovis; STRAIN=AF2122/97;
SPECIES-M. Dovis; STRAIN=AF2122/97;
MEDLINE=22709107; PubMed=12788972;
MEDLINE=22709107; PubMed=12788972;
MEDLINE=22709107; S. Grondin S., Lacroix C., Monsempe C., Simon S., Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R. Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R. Parkhill J., Barriell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003)
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19.3%; Pred. No. 0.025;
ive 67; Mismatches 111; Indels 114;
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388 AA; 46062 MW; 5DED0263275A9B24 CRC64;
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Interpro; IPR000863; Sulfotransferase.
Pfam; PF00685; Sulfotransfer; 1.
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EMBL; AE007076; AAK46611.1; -.
EMBL; BX248342; CAD97151.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 HNITRGKGMGD-HAFHTNARDALNVSQAWRWSLPYEKVSRLQKACG-DAMNLLGY----R 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 -EYLKLSSFGDRRILKKKKAVDNRSV-ETWRTELTIÉEMQTVTDLVGADILVELGYEQSIQ 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 -PRAHCRLLCSQQPFEVVEKACRSYSHVVLKEVRFFNLQSLYPLLKDPSLNLHIVHLVRD 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 VRDLIRAVFLCDMSVFDAYMEPGPRRQSSLFQWENSRALCSAPACDIIPQDEII-----
                                                                                MEDILINE=97361801; PubMed=9218762; Hanin M., Jabbouri S., Quesada-Vincens S., Freiberg C., Perret X., Hanin M., Jabbouri S., Quesada-Vincens S., Freiberg C., Perret X., Suromitron W.J., Fellay R.; "Sulphation of Rhizobium sp. NGR234 Nod factors is dependent on noeE, an new host-specificity gene."; Mol. Microbiol. 24:1119-1129(1997).
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                                                                                                                                                                                                                         MEDLINE-97305956; PubMed-9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
Perret X.;
                                                                                                                                                                                                                                                                                                     Nature 387:394-401(1997).
-!- FUNCTION: REQUIRED FOR THE FORMATION OF SULFATED NOD FACTOR. PROPOSED TO TRANSFER ACTIVATED SULFATE (PAPS) TO THE FUCOSE OF THE NOD FACTOR.
-!- SIMILARITY: LIMITED TO NODH AND TO C.ELEGANS F4269.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103;
                                                                                                                                                                                                                                                                                      "Molecular basis of symbiosis between Rhizobium and legumes.";
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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InterPro; IPR000863; Sulfotransferase.
Pfam, PF00685; Sulfotransfera; 1.
Nodulation; Transferase; Plasmid.
SEQUENCE 419 AA; 46569 MW; 848C48E0416AAA1F CRC64;
                   Rhizobium/Agrobacterium group; Rhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Mismatches 134;
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21.5%; Pred. No. 0.26;
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ses 78; Conserv
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SEQUENCE FROM N.A.
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                                    NCBI_TaxID=394;
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MEDINE-98044033; PubMed=3984377;

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Xunst F., Ogasawara N., Moszer I., Bolotin A., Borchert S.,

Ravedo V., Bertero M.C., Besslees P., Bolotin A., Borchert S.,

Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,

Browillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Ra Brouillet S., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

Ra Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

Ra Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

Ra Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

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Ra Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,

Rooris B., Karamata D., Kashara Y., Klaerr-Blanchard M., Klein C.,

Rooris B., Karamata D., Kashara Y., Klaerr-Blanchard M., Klein C.,

Rooris B., Karamata D., Koningstein G., Krogh S., Kumano M.,

Rooris B., Karamata D., Koningstein G., Krogh S., Kumano M.,

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Rooris B., Coll I.M., Portetelle D., Porwollik S., Resymolds S.,

Raper M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y.,

Rato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

Rato T., Scanlan E., Schleich S., Seror S., Shin B.S.,

Rato T., Scanlan S., Yandenbol M., Vanner P., Vansarotti A.,

A Tosato V., Uchlyama S., Vandenbol M., Vanner P., Vasarotti A.,

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Whitters P., Wipat A., Yamanot M. K., Yanner C., Yashikawa H.F., Zumstein E., Yoshikawa H.P., Zumstein E.,
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                                                                                                                                                                             Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                     Surfactin synthetaee subunit 1.
SRFAA OR SRFA1 OR SRFA OR BSU03480.
Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINE=97124189; PubMed=8969502;
                 P27206;
01-AUG-1992 (Rel. 23, Created)
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------AVIEPAEKQEHYPLHWHSSEHIS 1073
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                                                                                                                                74 PAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRROSSLFQWENSRALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 QQPFEVVEKACRSYSHVVLKEVRFFNLQSLYPLLKDPSL----NLHIV-----HLVRDPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1074 SASSEMRESAIHASSSNSEGFRYSKAGARISGINPTPRVIETSFVLENSTPROKIH-VCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209 AVFRSRERTKGDLMID--SRIVMGQHEQKLKKEDQPYYVMQVICQSQLEIYKTIQSLPKA
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N -> F (IN REF. 1).
S -> A (IN REF. 1).
S -> R (IN REF. 1).
S -> X (IN REF. 1).
S -> Y (IN REF. 1).
HQWSHPPFTTSH. -> DEMSDAGLFTRSE (IN REF.
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E -> R (IN REF. 1).
W, BC02FB157D7F1FDB CRC64;
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(3)
V -> L (IN REF. 1 AND 5

G -> A (IN REF. 1).

Q -> T (IN REF. 1).

D -> T (IN REF. 1).

A -> P (IN REF. 1).

Y -> I (IN REF. 1).

Y -> I (IN REF. 1).

PT -> GS (IN REF. 1).

P -> R (IN REF. 1).
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Best Local Similarity 19.7
Matches 63; Conservative
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                                                                                                                                      STRAIN=168;
MEDLINE=95219080; PubMed=7704255;
Fulshima Y., Yamane K.;
"A 10 kb nucleoride sequence at the 5' flanking region (32 degrees)
of srfAA of the Bacillus subtilis chromosome.";
Microbiology 141:277-279(1995).
                                                                                                                                                                                                                                            SEQUENCE OF 1-38 FROM N.A.
MEDLINE-91358326; PubMed=1715856;
MARAIO M.M., Xia L., Zuber P.;
"Transcription initiation region of the srfA operon, which is controlled by the comP-comA signal transduction system in Bacillus
                                                                                                                                                                                                                                                                                                                                    "Bacteriol, 173:5487-5493 (1991).

-!- FUNCTION: THES PROTEIN IS A MULTIFUNCTIONAL ENZYME ABLE TO

-- FUNCTION: THES PROTEIN IS A MULTIFUNCTIONAL ENZYME ABLE TO

ACTIVATE AND POLYMERIZE THE AMINO ACIDS LEU, GLU, ASP AND VAL.

ACTIVATION SITES FOR THESE AA CONSIST OF INDIVIDUAL DOMAINS.

-- COFACTOR: CONTAINS 3 COVALENTLY DOUND Phosphopantethelines.

--- PATHWAY: Gyclic peptide antibiotic surfactin biosynthesis.

--- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR006163; Pp_bind.
InterPro; IPR006162; Ppaintne S.
Pfam; PF00501; AMP-binding; 3.
Pfam; PF00550; pp-binding; 3.
Pfam; PF00550; pp-binding; 3.
PROSITE; PR00124; AMPENINDING;
PROSITE; PS00012; PHOSPHOPANTETHEINE; 2.
PROSITE; PS00455; AMP_BINDING; 3.
PROSITE; PS00455; AMP_BINDING; 3.
PROSITE; PS00455; AMP_BINDING; 3.
Iniquee; Antibiotic blosynthesis; Phosphopantetheine; Sporulation;
                                                        "srfA is an operon required for surfactin production, competence development, and efficient sporulation in Bacillus subtilis."; J. Bacteriol. 173:1770-1778(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al enzyme; Repeat; Complete proceome.
? 1047 DOMAIN ! (GLU-ACTIVATING).
? 3115 DOMAIN 2 (LEU-ACTIVATING).
? 3115 DOMAIN 3 (D-LEU-ACTIVATING).
? 3080 ACYL CARRIER (ACP) 1.
31 2080 ACYL CARRIER (ACP) 2.
44 3110 ACYL CARRIER (ACP) 2.
906 1006 PHOSPHOPANTETHEINE (POTENTIAL).
913 2043 PHOSPHOPANTETHEINE (POTENTIAL).
914 3074 M -> I (IN REF. I AND 5).
                 MEDLINE=91154134; PubMed=1847909;
Nakano_M.M., Magnuson R., Myers A.M., Curry J., Grossman A.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - SIMILARITY: Contains 3 acyl carrier domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; 299105; CAB12142.1; --
EMBL; M59939; AAA22815.1; --
EMBL; M64702; AAA22816.1; --
PIR; 140485; 140486.
HSSP; P14687; 1AMU.
Subtlists; BG10168; srfAA.
InterPro; IPR00193; AMP-bind.
InterPro; IPR001242; Condensatn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D13262; BAA02522.1; -. EMBL; X70356; CAA49816.1; -. EMBL; D50453; BAA08982.1; -.
    SEQUENCE OF 1-460 FROM N.A.
                                                                                                                         SEQUENCE OF 1-64 FROM N.A.
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Ohāra O.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 IDSRIVMGQHEQXLKKEDQPYYVMQVICQSQ----LEIYKTIQSLPKALQERYLLVRXED 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 RSGSSFVGQLFGQHPDV----FYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 VFDDAV-----LCNKDP-----SAFITELVAXHSELAPR----LCNKDP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDEISMFVQWNQELRK-----YER
                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
LUMENAL, CATALYIC (POTENTIAL).
9PC2F44539B8CC53 CRC64;
                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caehorhabditis.
                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the protein sulfotransferase family.
                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Transferase; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
      30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Putative protein-tyrosine sulfotransferase (EC 2.8.2.20)
(Tyrosylprotein sulfotransferase) (TPST).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 2.4;
48; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.5%; Score 92;
19.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                          WormPep; F42G9.8; CE07235.
InterPro; IPR000863; Sulfotransferase.
Pfam; PF00685; Sulfotransfer; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      41469 MW;
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                                                                    Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                   PIR; T16350; T16350
                                                                                                                                                                                                                                                                                                                                                                                                                                     359 AA;
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Matches 63; Conserv
                                                                                                                   SEQUENCE FROM N.A.
STRAIN-Bristol N2;
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                                                                                                NCBI_TaxID=6239;
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                30-MAY-2000 (
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SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE20001959; Pubmed=10529403;
MEDLINE220001959; Pubmed=10529403;
Okuda T., Matsuda S., Nakatsugawa S., Ichigotani Y., Iwahashi N.,
Takahashi M., Ishigaki T., Hamaguchi M.; homologue of Drosophila
"Molecular cloning of macrophin, a human homologue of Drosophila
"Makapo with a close structural similarity to plectin and dystrophin.";
Biochem. Biophys. Res. Commun. 264:568-574(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-22158633; PubMed=12168954;
Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
"Construction of expression-ready cDNA clones for KIAA genes: manual
curation of 330 KIAA cDNA clones.";
DNA Res. 9:99-106(2002).
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                             OSUDNI; O75053; Q8WXY2; Q9H540; Q9UXP0; Q9ULG9; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Microtubule-actin crosslinking factor 1, isoforms 1/2/3 (Actin crosslinking family protein 7) (Macrophin 1) (Trabeculin-alpha) (620 kDa actin-binding protein) (ABP620). How Sapiens (Human).
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Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,
Nakejima D., Nomura N., Ohara O.;
"Characterization of cDNA clones in size-fractionated cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "prediction of the coding sequences of unidentified human genes. XV Ine complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20026884; PubMed=1055937; Sun Y., Zhang U., Kraeft S.-K., Auclair D., Chang M.-S., Liu Y., Sun Y., Zhang U., Kraeft S.-K., Auclair D., Chang M.-S., Liu Y., Sutherland R., Salgia R., Griffin J.D., Ferland L.H., Chen L.B.; Molecular cloning and characterization of human trabeculin-alpha, giant protein defining a new family of actin-binding proteins."; J. Blol. Chem. 274:33522-33530(1999).
                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Rutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Res. 4:345-349(1997).
Res. 4:345-349(1997).
FUNCTION: F-actin-binding protein which may play a role in c Function. Fractin-binding protein which may play a role in c linking actin to other cytoskeletal proteins. Also binds to microtubules (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 182-4812 FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE=21833812; PubMed=11845288; Goog T.-W.L., Besiril C.G., Lomax M.I.; "MACFI gene structure: a hybrid of plectin and dystrophin."; Mamm. Genome 12:852-861(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND ALTERNATIVE SPLICING
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5430 AA
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MEDLINE=20039619; PubMed=10574462;
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SEQUENCE OF 1544-5057 FROM N.A.
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DNA Res. 6:337-345(1999).
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STANDARD;
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DNA Res. 4:345-349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 FGQHPDVFYLMEPAWHVWMTFKQSTAWMLHM-AVRDLIRAVFLCDMSVFDAYMEPGPRRQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 SSLFQWENSRALCSAPACDIIPQDEIIPRAHCRLLCSQQPF--EVVEKACRSYSH---- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1752 LLSQQQNFILATQSAQA----FLDQHGHNLT-----PEEQQML-----QQKLGEL
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22.2%; Pred. No. 78;
:ive 66; Mismatches 128; Indels 115;
                     (POTENTIAL)
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Best Local Similarity 22.2%
Matches 88; Conservative
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## BMBL; AF325339; AAL38997.1; JOINED.

## BMBL; AF325340; AAL38997.1; JOINED.

## CO: GO:10005593; F:Galzum ion binding; ISS.

## CO: GO:10005593; F:Galzum ion binding; ISS.

## CO: GO:10005593; F:Galzum ion binding; ISS.

## Inceptor IPRO2009; Embard.

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                                                                                                                                                                                                                                                                                                            | : :::: : | : | | 1874 FVIISGQKVLDMENSFKEGKEPS---EIGNLVKD-----KLKDATERYTALHSKCTRLGS 1925
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                                                                                                                                                                                                                                                                           174 -VVLKEVRFFNLQSLYPLLKDPŞLNLHIVHLVRDPRAVFRSRERTKGDLMIDSR---- 226
                                                                                                                                                                                                                                                                                                                                                                                      227 ---IVMGQHEQKLKKEDQPYYVMQVICQSQLE--IYKTIQSLPKALQERYLLVRYEDLAR
                                                                                                                                                                                                                                                                                                                                                                                                                      Isold=Q9UPN3-3; Sequence=External;
TISSUE SPECIFICITY: Expressed in heart, lung, pituitary and
placenta, not found in brain, kidney, liver, pancreas or skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAC4 HUMAN STANDARD; PRT; 5938 AA.

MO96PK2; Q8WXX1;
10-OCT_2003 (Rel. 42, Last sequence update)
10-OCT_2003 (Rel. 42, Last sequence update)
10-OCT_2003 (Rel. 42, Last annotation update)
Microtubule-actin crosslinking factor 1, isoform 4.

MACF1 OR ACF7 OR ABP620 OR KIAA0465 OR KIAA1251.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Fig. TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: Belongs to the plakin or cytolinker family.
-1- SIMILARITY: Contains 2 Br-hand calcium-binding domains.
-1- SIMILARITY: Contains 19 plectin repeats.
-1- SIMILARITY: Contains 32 spectrin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2032 SLA-ERSSLLOKAIAOS------OSVOESLESLL 2058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337 SLPYEKVSRLOKACGDAMNLLGYRHVRSEQEQRNLLL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=4;
IsoId=096PK2-1; Sequence=Displayed;
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Name=1;
Isold=Q9UPN3-1; Sequence=External;
Name=2;
Isold=Q9UPN3-2; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF317696, AAL09459.1; -...
EMBL, AF325341; AAL38997.1; -...
EMBL, AF32533; AAL38997.1; JOINED.
EMBL, AF325334; AAL38997.1; JOINED.
EMBL, AF325335; AAL38997.1; JOINED.
EMBL, AF325336; AAL38997.1; JOINED.
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                                                                                                                                                                                                                                                                      TISSUE_Colon, Kidney, and Stomach;

TISSUE_Colon, Kidney, and Stomach;

TISSUE_Colon, Kidney, and Stomach;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Morer T., Max S.I., Wang J., Hsieh F.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Stapleton M., Saares W.B., Bonaldo M.F., Casavant T.L., Scheetz T. E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Richards S.W., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.",

"Insure Specificity: Expressed Predominanty IN Fetal Brain.

"Insurant Acad Sci. U.S.A.

"Insurant Acad Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 DIIPODEIIPRAHCRLLCSQOPFEVVEKACRSYSHVVL------KEVRFFNLQSL 187
[1]
SEQUENCE FROM N.A.
MEDLINE=95080775; PubMed=7527372;
SCHWATLZ F., Neve R., Eisenman R., Gessler M., Bruns G.;
SCHWATLZ F., Neve between PAX-6 and FSHB expressed in fetal brain.";
"A WAGR region gene between PAX-6 and FSHB expressed in fetal brain.";
Hum. Genet. 94:658-664(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 YPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDSRIVM-GQHEQKLKKE----D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPYYVMQVICQSQLEIYKTIQSLPKALQERYLLVRYEDLARAPVAQTSRM----YBFVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LINSIYLQDSEVTVKGFRIYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90; Gaps
                                                                                                                                                                         Schwartz F., Eisenman R., Knoll J., Gessler M., Bruns G., Eisenman R., Knoll J., Gessler M., Bruns G., Eloya sequence, genomic organization, and evolutionary conservation of a novel gene from the WAGR region."; Genomics 29:526-532(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Pram; PF00149; Metallophos; 1.
SEQUENCE 294 AA; 33360 MW; 43B2BC0DA1BFD1F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.5%; Score 91; DB 1
20.2%; Pred. No. 2.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; GO:0007399; P:neurogenesis; TAS.
                                                                                                                              LZJ
SEQUENCE FROM N.A.
MEDLINE=96115606; PubMed=8666403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC031582; AAH31582.1; -.
Genew; HGNC:1180; Cllorf8.
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Best Local Similarity
Matches 53; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 FGQHPDVFYLMEPAWHVWMTFKQSTAWMLHM-AVRDLIRAVFLCDMSVFDAYMEPGPRRQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 -VVLKEVRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDSR----- 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 APVAQISRMYEFVGLEFLP--HLQTWVHNI--TRGKGMGDHAFHTNARDA-LNVSQAWRW 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IVMGQHEQKLKKEDQPYYVMQVICQSQLE--IYKTIQSLPKALQERYLLVRYEDLAR 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2428 HLNMLLGQYHQFQNSADSLQAWMQA-CEANVEKLLSDTVASDPGVLQEQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2295 KEÓYS----TSLAÓSEAELKQVQTLQDELQK-FLQDHKEFESWLE---RSE
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.5%; Score 91.5; DB 1; Length 5938; 22.2%; Pred. No. 87; ative 66; Mismatches 128; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; AAL38997).
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SPECTRIN 32.
P -> S (IN REF. 1; AAL38997)
WW; B8784112752DA004 CRC64;
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15-771-1998 (Rel. 36, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-BAR brain protein 239 (239FB).
CIIORF8 OR FAMIB.
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SPECTRIN 29.
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5091 SPEC
5309 SPEC
5309 SPEC
5418 SPEC
5555 SPEC
1712 P ->
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4211
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Best Local Similarity
Matches 88; Conserv
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Q15777;
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68 VEYIMEPAWHVWMTFKQSTAWMIHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQSSLFQWE
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                                                                                                                                                                                                                                                                      249 ICQSQLBIYKTIQSLPKALQERYLLVRYEDL------ARAPVAQTSRMYEFVGL
                                                                                                                                                                  528 IIYCODOIYR-----KALOK----VREBEAEBERKHGKSRSAOSPNLOTSSMD----
                                                                                                                        201 VHLVRD-PRAVFR-----SRERIKGDLMIDSRIVMGQHEQKLKKEDQPYYVMQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine. NCBI_TaxID=3847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIANESON G3; MEDIANESON G3; MEDIANESON G3; MEDIANESON G3; MEDIANESON G3; MEDIANESON G4; MEDIANESON G5; MEDIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 504;
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504 AA, 57579 MW, 86E4FAEEC2FF2A8F CRC64;
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4.4%; Score 89.5; DB 1;
Best Local Similarity 19.9%; Pred. No. 5.9;
Matches 70; Conservative 45; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-2003 (Rel. 42, Last annotation update)
Cytochrome P450 71D8 (EC 1.14.-.-) (P450 CP7).
CYP71D8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504 AA
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INTERPRO; IPR001J28; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        297 EFLPHLOTW---VHN 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIFOHLNAYROBAHN 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOYBN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C7D8_SOYBN
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-i- SIMILARITY: Belongs to the dynamin family.

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or send an email to license@isb-sib.ch.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 ELQKYGADIPEDENEKTLFLIEKINAF-NQDITAİVEGEEİVREKECRLFTKLRKEFFLW 412
                    EFLPHLQTWVHNITRGKGMGDHAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMNL 356
                                                                                           ----KWNLIPEGIDILM-THGPP--- 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 FKEHPQFRALLEDG-----KATVPCLAERLIMELISHICKSLPLLENQIKESHQSTSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR, $11737, $11737.

PIR, $11737, $11737.

InterPro; IPR001401; Dynamin.

InterPro; IPR001375; Dynamin.

Pfam; PF00350; dynamin.; 1.

Pfam; PF00131; dynamin.; 2, 1.

Pfam; PF00132; dynamin.; 2, 1.

Pfam; PF00135; DYNAMIN.

SMART; SM00053; DYNC; 1.

SMART; SM00053; DYNC; 1.

PROSITE; PS00410; DYNAMIN, 1.

INTERFERON induction; GEP: binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74951 MW; F55D63283BC865B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Interferon-induced GTP-binding protein Mx3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     659 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -EVVEKACRSYSHVVLKEVRFFNLQ---
                                                                                                                                                                          LGYRHVRSEQEQRNLLLDLLST 378
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LGFRDWVPKELQRVGCVELLNT 238
                                                                                       PWTPWFNGWGFNLPRGOSLLD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Best Local Similarity
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                    297
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                                                                                                                                                                      357
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SEPTER SOOS SEPTER SEPT

8 8 8 8 8

SIMILARITY: Contains 4 acyl carrier domains.

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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Ractero M.G., Bessieres P., Bolotin A., Borchert S., Barsiser I., Brans A., Braum M., Brignell S.C., Bron S., Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., A. Brouillet S., Brisch E., C., Bron S., Brisch S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Britan K.D., Errington T. Britan K.D., Darierfolf A., Ehrlich S.D., Emmerson P.T., R. Britan K.D., Errington J., Funa S., Galizzi A., Galleron N., A. Eritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., A. Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., A. Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Mell C., A. Liu H., Masude C., Medique C., A. Liu H., Masude C., Medique C., A. Medina M., Mellado R.P., Mizuno M., Mosetl D., Nakai S., Noback M., Anone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Roone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Rey M., Reynolds S., Rieger M., Ravolde C., Rocha E., Pulic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Reiger M., Tacconi E., Pulic B., Rapoport G., Rosen M., Sadaie Y., Rocha E., Schleich S., Schroeter R., Scoffone F., Schleich S., Aramaco H., Vannier F., Vasearott A.M., Vannier P., Wambutt R., Wedler E., Weller E., Wedler E., Weller E., Wedler E., Weller E., Wedler E., Weller E., Weller E., Weller E., Rose M., Berri W., Danchin A., Tarken E., Perken E., Pe
                                                                                                                                                                                                      | | : | | | : | | | : | | | 190 FGKENDDQDEFWSLVRKAITWTGGFEVDDMFPSLKP-LHLLTRQKAKVEHV-HQRADKIL 247
                                                                                                     245 VMQVICQSQLEIYKTIQSLPKALQE--RYLLVRYEDLARAPVAQTSRMYEFVGL-----
                                                                                                                                                                         - PHLQTWVHNITRGKGMGDHAFHTNA - - - -
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TOGNOIA A., Grandi G.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POTENTIALLY INVOLVED IN SOME INTERMEDIATE STEPS FOR THE SYNTHESIS OF A POLYKETIDE MOLECULE WHICH MAY BE INVOLVED IN
                                                                                                                                                                                                                                                                                                 -----SEAEQEDLVDVLL 279
                                                                                                                                                                                                                                                                    325 RDALNVSQAWRWSLPYEKVSRLQKACGDAMNLLGYRHVRSEQEQRNLLLDLL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECONDARY METABOLISM. COPACTOR: Contains 4 covalently bound phosphopantetheines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative polyketide synthase pksM.
PKSM OR PKSY OR BSU17200.
Bacillus subtilis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PKSM BACSU STANDARD; PRT; 4273 AA. P40872; 031781; 01-FEB-1995 (Rel. 31, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                   248 EDILRKHM------EKRIRVKEGNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 YEDLARAPVAQT-SRMYE-----FVGLEFLPHLQTWVHNIT--RGKGMGDHAFHTN 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heine; Multifunctional enzyme; Repeat; Complete proteome.

364 ACYL CARRIER (ACP) 1.

96 834 BETA-KETOACYL SYNTHASE 1.

22 2737 BETA-KETOACYL SYNTHASE 2.

23 2737 BETA-KETOACYL SYNTHASE 3.

10 3483 ACYL CARRIER (ACP) 3.

40 4209 ACYL CARRIER (ACP) 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 TKGDLMIDSRIVMGQHE-QKLKKEDQPYYVMQVICQSQLEIYKTIQSLPKALQERYLLVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 FEVVEKACRSYSHVVLKEVRFFNLOSLYPLLKDPS----LNLHIVHLVRDPRAVFRSRER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHOPANTETHEINE (POTENTIAL).
PHOSPHOPANTETHEINE (POTENTIAL).
BETA-KETOACYL SYNTHASE (BY SIMILARITY).
PHOSPHOPANTETHEINE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHOPANTETHEINE (POTENTIAL).
BETA-KETOACYL SYNTHASE (BY SIMILARITY).
PHOSPHOPANTETHEINE (POTENTIAL).
                                                                                                                                                                                            R PIR; C56679; C65679.
R Subtilist, BG10391; pksM.
R InterPro; PRR001994; Ketoacyl_synth.
R InterPro; IRR001994; Ketoacyl_synth.
R InterPro; IRR001601; Methyltransf.
R InterPro; IRR001601; Methyltransf.
R InterPro; IRR00161; Ppinde.
R InterPro; IRR00161; Ppinde.
R InterPro; IRR00161; Spantne S.
R Pfam; PF001106; adh Short; 1.
R Pfam; PF001109; ketoacyl-synt; 3.
R Pfam; PF00109; ketoacyl-synt; 3.
R Pfam; PF00500; pp-linding; 4.
R PROSITE; PS00012; PHOSPHOPANTETHEINE; 2.
R PROSITE; PS00012; PHOSPHOPANTETHEINE; 2.
R PROSITE; PS00015; AGCP DOMAIN; 4.
R TRANSferase; Acyltransferase; Antiblotic biosynthesis; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.4%; Score 89.5; DB 1; Length 4273; 22.9%; Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 E -> V (IN REF. 2).

76 Q -> E (IN REF. 2).

89 T -> S (IN REF. 2).

477459 MW, 3BBFCF1A250ABB5A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              324 ARDALNVSQAWRWSLPYEKVS---RLQKAC 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F4ST FLACH STANDARD;
P52837;
01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                               EMBL; Z99113; CAB13603.1; -. EMBL; Z35133; CAA84505.1; -. PIR; C69679; C69679.
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3690
4172
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F4ST FLACH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --MATHMPYH 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 VVEKACRSYSHVVLKEVRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLM 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVSFYHFGREITKLPLEDAPFE-----EAFDEFYHGISQFGPYWDHLLGYWKASLERPE 210
                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=92159034; PubMed=1741382;
Varin L., Deluca V., Ibrahim R.K., Brisson N.;
"Molecular characterization of two plant flavonol sulfotransferases.";
Proc. Natl. Acad. Sci. U.S.A. 89:1286-1290(1992).
                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids, campanulids, Asterales, Asteraceae, Asteroideae, Tageteae, Flaveria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 MEP------GPRRQSSLFQ-WENSRALCSAPACDIIPQDEIIPRAHCRLLCSQQPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --KALQER--
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                                                                                                                                                                                                                                                                                                                                                                   MEDINE-95279378; Pubmed=7759495;
Varin L., Marsolais F., Brisson N.;
"Chimeric flavonol sulfortansferases define a domain responsible for substrate and position specificities";
J. Biol. Chem. 270:12499-12502(1955).
-!- FUNCTION: Transfers sulfate group into flavonolin position 4'.
May play a role in auxin transport.
-!- STBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: Highest in shoot tips and lowest in mature leaves and rocts (8y similarity).
-!- SIMILARITY: Belongs to the plant sulfotransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100;
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Flavonol 4'-sulfortransferase (EC 2.8.2.-) (F4-ST).
Flavoria chloraefolia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -YLLVRYEDLARAPVAQTSRMYEFVGLEF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 VILFLKYEDVKKDPTSNVKRLAEFIGYPF 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.4%; Score 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000863; Sulfotransferase.
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37255 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M84136; AAA33343.1; -.
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                                                                                                                                                                                                                                                                                                                                                         PAPS-BINDING SITE.
                                                                                                                                                                    NCBI_TaxID=4228;
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MPPA_RAT
ID _MPPA_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311
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                                                                                                                                                                              Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITOCHONDRIAL PROCESSING PEPTIDASE
                                                                              mitochondrial
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InterPro, IPR007863; Peptidase_M16_C.
Pfam; PF00675; Peptidase_M16; 1.
Pfam; PF05193; Peptidase_M16 c; 1.
PR051TE; PS01043; INSULINASE; 1.
Hydrolase; Metalloprotease; Mitochondrion; Transit peptide.
TRANSIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 524;
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last senocation update)
Mitochondrial processing peptidase alpha subunit,
precursor (EC 34.4.64) (Alpha-MPP) (P-55).
PMPCA OR INPPES OR MPPA.
Ratters norvegicus (Raf).
                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.4%; Score 89;
21.5%; Pred. No.
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MEROPS; M16.971; -.
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MEROPS; C23.001; -.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=12168;
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NP BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     734
QTSRMYEFVGLEFLPH-LQTWVHNITRGKGMGDHAFHTNARDALNVSQAWRWSLPYEKVS 344
                         ---KPEDIKRVASKMLRGKP---- 488
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-SERIOR OF ARCC 700294 / Serotype M1;
MEDLINE-SI192684; PubMed=11296296;
Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Sezare S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; Song L., White J.,
"Complete genome sequence of an MI strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S., 98:4658-4663[2001].

-I-FUNCTION: Through the carboxylation of phosphoenolpyruvate (PEP)
it forms oxaloacetate, a four-carbon dicarboxylic acid source for
the tricarboxylic acid cycle.
-I-CANALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | | : | | : | | : | | : | | : | | : | | ITDPNEIDSFRE-IMDSIVADSNIIY----RKL-VFDNPHFYDYFFEASPI---KEVSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 VRDPRAVFRSRERTKGDLMIDSRIVMGQHEQKLKKEDQPYYVMQVICQSQLEIYKTIQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82;
                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCase) (PEPC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 920;
14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRODISO; PEPCARRYLASE.
PROSITE; PS00781; PEPCASE 1; 1.
PROSITE; PS00383; PEPCASE 2; 1.
Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                      Streptococcus pyogenes.
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           583 583 BY SIMILARITY.
920 AA; 104751 MW; 464EA4A309A22237 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphoenolpyruvate + CO(2).
-!- PATHWAY: Tricarboxylic acid cycle.
-!- SIMILARITY: Belongs to the PEPCase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.4%; Score 89; DB 1
18.6%; Pred. No. 14;
tive 48; Mismatches
                                                                                                                                               920 AA.
           THSKK-----LPHELCTLIRNV-----
                                                                    489 -AVAALGDLTDLPTYEHIQAALSSRD 513
                                                   345 RLOKACGDAMNLLGYRHVRSEQEORN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY
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HSSP; P00864; 1FIY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP, MF 00595; -; 1.
InterPro; IPR001449; PEPcase.
Pfam; PF00311; PEPcase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 18.6%
les 49; Conservative
                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                               NCBI_TaxID=1314;
                                                                                                                                               STRPY
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ACT_SITE
SEQUENCE
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                           455
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and its statement is not removed. Usage by and for commercial entities a pricense agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                               68
                                            309 --ITRGKGMGD---HAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDA-MNL-LGYRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P17955, Q89548;
UNOV-1990 (Rel. 16, Created)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
RNA replication protein (147 kDa protein) (ORF 1) [Contains: RNA-discrete RNA polymerase (EC 2.7.7.48); Probable helicase].
Potato virus M (strain Russian) (VPM).
Viruses; SSRNA positive-strand viruses, no DNA stage; Flexiviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Gen. Virol. 72:9-14(1991).
-!- FUNCTION: RNA-replication. The central part of this protein
possibly functions as an ATP-binding helicase.
-!- ÇATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 126;
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4.4%; Score 89; DB 1; Length 1968;
Best Local Similarity 20.7%; Pred. No. 36;
Matches 71; Conservative 38; Mismatches 108; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1166 1173 ATP (POTENTIAL)
1968 AA; 223384 MW; 6F15A79E1AD96AAC CRC64;
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264 PKALQERYLLVRYEDLARAPVAQTSRMYEFVGLEFLPHLQTWVHN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91116326; PubMed=1990070;
Zavriev S.K., Kanyuka K.V., Levay K.E.;
"The genome organization of potato virus M RNA.";
J. Gen. Virol. 72:9-14(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1968 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 OTU domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEMORS; CZO. 1PR00323; OTU.
InterPro; IPR008041; Peptidase C23.
InterPro; IPR001708; RNA dep RNAP012.
InterPro; IPR007095; RNA DOI DS PS.
InterPro; IPR007094; RNA DOI PSVIT.
InterPro; IPR000666; Viral_helicase1.
                                                                                                                                                                                                                                                                                                                         Pfam, PF02338; OTU; 1.
Pfam, PF05379; Peptidase_C23; 1.
Pfam; PF00978; RNA, dep RNApol2; 1.
Pfam; PF01443; Viral_helicase1; 1.
                                                                                                                                                                                                                                                                         362 VRSEQEQRNLLLDLLSTWTVPEQI
                                                                                                                                                                                                         780 RYIDRAQGNLERLQHMYQT----
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414	116	453	166	510	225	545	277	595			
367 FARLVIHN-SSMCATIMPEQLKEFMGNWLGKMPSVLARRFSSVRAVCVN 414	9FYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPG	415 KFIRGLKPYSFTLRLNEITWWNIWENSYAWFFDTDAEVD 453	117 - PRRQSSLFOWENSRALCSAPACDIIPODBIIPRAHCRLLC-SQOPFEVVEK	VPEKLDSLFMGEGAGLVAHITSRPYVGTVPLADREWNALLCMDSQKLLHAMRRMFMR	7 - ACRSYSHVVLKEVRFENLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDS	511 GAWGAHMCVISREFLLKYVEARLKSSCLIAKARRR	KLKKEDOPYYVMQVIC	5GOHKEKLEAWEVLGIKSSDALFRAMTYLCNARLEPMFSESGLRFFLTRGR	DLARAPVAQTSRMYEFVG	596 NNLYGLINYTEGKRAVTGVQNLWSNVVHEVSTKRHKGM 633	
36.	69	415	11.	454	167	511	22(546	278	296	
do do	٥٧	QQ	ò	qq	à	QΩ	ò	qq	à	QC	

Search completed: May 6, 2004, 10:50:27 Job time: 19 secs

4007 95:05:TT 9 inu may

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

6, 2004, 10:47:22 ; Search time 44 Seconds Run on:

(without alignments) 2767.955 Million cell updates/sec

US-09-645-078-2 2038 1 MLDPKKWKLLLFLVSQMAIL.......BQRNLLLDLLSTWTVPEQIH 386

Title: Perfect score:

Sequence:

Scoring table:

1017041 segs, 315518202 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL 25:* Database

sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_varceriap:* sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_human:*
sp_mammal:*
sp_mammal:* sp_mnc:*
sp_organelle:*
sp_phage:*
sp_plant:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

	sapien	sapien	sapien	musculu	musculu	sapien	musculu	sapien		musculu	sapien	sapien	musculu	musculu	sapien	sapien
Description	Q9y5r3 homo	Q8ncg5 homo	Q8iv46 homo	Q9rlil mus	Q9wue5 mus	OBGZX3 homo	Q9qup4 mus	Omod 68zg60	Q9ep78 mus	Snm 0qu660	075667 homo	Q9ns84 homo	O88276 mus	Q80wv3 mus	Ogneds homo	Q9y4c5 homo
ΩI	Q9Y5R3	QBNCG5	Q8IV46	Q9R111	Q9WUE5	Q9GZX3	Q9QUP4	68Z56Ö	Q9EP78	09NB0	075667	Q9NS84	088276	Q80WV3	Q9UEDS	Q9Y4C5
DB	4	4	4	17	11	4	11	4	I	11	4	4	H	11	4	4
% Query Match Length D	386	386	370	388	388	395	395	411	484	484	486	486	530	530	483	530
% Query Match	100.0	99.9	96.3	74.4	74.3	50.0	49.9	49.5	30.8	30.6	29.8	29.7	29.4	29.5	29.0	29.0
Score	2038	2035	1963	1515.5	1513.5	1019	1017.5	1008	627	624	606.5	605.5	598.5	595.5	591.5	591.5
Result No.	 	7	m	4	ιO	9	7	80	9	10	11	12	13	14	15	16

enm o	рошо	enm 6	homo saj	rattus	ന	dros	5 mus musc	drosophil	Q8mzd1 drosophila	Q95ja8 oryctolagus		_	_			halocy	O9bgx0 macaca fasc	homo	homo	2	7	모		a	xant	2 homo sapi	е еше	Q9uvp2 emericella
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09EQC0	043916	088199	075099	Q9QZL2	093403	Q9VMC3	Q9DOK5	Q9VMC4	Q8MZD1	Q95JA8	092VG4	QBPRAO	QBAAPB	Q7UP52	Q93JE6	Q86R90	Q9BGX0	QBIZUB	Q9P2D3	Q96QU2	080067	090011	Q8VZE	Q84RR2	O8KWX0	Q9H0K2	95VU60	Q9UVP2
11	4	Н	4	11	13	ß	н	ហ				16		16	16	Ŋ	φ	4	4	4	17	4	10	10	(1	4	m	т
4.11	411	472	479	474	441	486	120	363	363	119	307	274	368	413	303	360	655	1222	1586	747	762	775	593	593	285	743	2454	2454
27.4	26.9			23.6	20.8	13.0		10.3	ø.	8.6	8.2	6.1	ъ. 8	5.7	5.7	9.5	5.4	5.3	5.3	6.4	4.	9.	4.	4.	8.8	4.7	4.7	4.7
559	549	504.5	482	481.5	23	~	215		σ	175	168	124.5	118	116.5	115.5	115	111	108.5	107	100.5	100.5	100.5	100	100	97.5	96.5	96	96
17	18	6	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	3.7	8	6 8	40	4	42	43	44	45

RESULT 1

SEQUENCE FROM N.A.

TISSUB=Tonsil;

MEDLINES99264336; PubMed=10330415;
Bistrup A., Bhakta S., Lee J.K., Belov Y.Y., Gunn M.D., Zuo F.R.,

Huang C.C., Kannagi R., Rosen S.D., Hemmerich S.;

"Sulfoctransferases of two specificities function in the reconstitution of high endotholial cell ligands for L-selectin.";

J. Cell Biol. 145:899-910(1999). [3] SOUDNICE FOR N.A. MEDINE21332592; PubMed=11439191; MEXAYAMA J., Ellies L.G., Yeh J.-C., Hiraoka N., Petryniak B., Nakayama J., Ellies L.G., Yeh J.-C., Hindsgaul O., Marth J.D., Lowe J.B., Fakuda M.; Rabuka D., Hindsgaul O., Marth J.D., Lowel and their control by a "Novel sulfated lymphocyte homing receptors and their control by a corel extension betal,3-N-acetylglucosaminyltransferase."; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-UNV-2003 (TrEMBLrel. 24, Last annotation update) N-acetylglucosamine 6-O-sulfotransferase (L-selectin ligand sulfotransferase GST-3). SECURNCE FROM N.A.
TISSUB=ronsil;
TISSUB=ronsil;
Remerich S., Lee J.-K., Bhakta S., Bistrup A., Ruddle N.R.
Rosen S.D.;
"Chromosomal Localization and Genomic Organization for the GalactoseAN-Acetylgalactosamine/N-Acetylglucosamine 6-O-Sulforransferase Gene Family.";
Glycobiology 0:0-0(2001). 386 AA PRT; PRELIMINARY; Q9Y5R3 Q9Y5R3;

GO; GO:0008146; F:sulfotransferase activity; IEA.
InterPro; IPR00865; Sulfotransferase.
Pfam, PF00685; Sulfotransfer; 1.
Hypothetical protein.
SEQUENCE 386 AA; 45160 NW; 861869348319E42A CRC64;

8 K R B S

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61 LFGQHPDVFYLMEPAWHVWNTFKQSTAWNLHWAVRDLIRAVFLCDMSVFDAYMEPGPRRQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 LFGQHPDVFYLMEPAMHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FFNLOSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDSRIVMGQHEQKLKKED 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 FFNLÖSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDSRIVMGQHEOKLKKED 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 QPYYVMQVICQSQLEIYKTIQSLPKALQERYLLVRYEDLARAPVAQTSRMYEFVGLEFLP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 OPYYVMOVICOSOLEIYKTIOSLPKALOERYLLVRYEDLARAPVAOTSRMYEFVGLEFLP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 HLQTWVHNITRGKGMGDHAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMNLLGYR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 SSLFQWENSRALCSAPACDIIPQDEIIPRAHCRLLCSQQPFEVVEKACRSYSHVVLKEVR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 HLQTWVHNITRGKGMGDHAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMNLLGYR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLLPKKMKLLLFLVSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFVGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLLPKKVKTLLFLVSQMAILALFFHWYSHNISSLSMKAQPERMFVLVLSSWRSGSSFVGQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

ISOGAI T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,

ISOGAI T., Ota T., Nishikawa T., Ishii S., Kawai-Hio Y., Saito K.,

Yamamoto Y., Nagai K., Sugamara Y., Kojima S., Nogahari K.,

Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,

Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

"NEDO human cDNA sequencing project.";

Submitted (MRA-2002) to the EMBL/GenBank/DDBJ databases.

Genew, HGNC:1972; CHST4.
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 24, Last sequence update)
01-UNY-2003 (TrEMBLRel. 24, Last sequence update)
Hypothetical protein FLJ90265.
Hypothetical protein FLJ90265.
Box Assarycta; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 2038; DB 4; Length 386; Best Local Similarity 100.0%; Pred. No. 5.5e-183; Matches 386; Conservative 0; Mismatches 0; Indels 0;
Cell 105:957-969(2001).

R EMBL, APR131255 AAA33015.1; -
R EMBL, APR49089; AAA48246.1; -
R EMBL, APR49089; AAA48246.1; -
R EMBL, APR49089; AAA482417.1; -
R GO; GO:0008146; F:sulfortransferase activity; TAS.
GO; GO:000726; P:cell adhesion; TAS.
GO; GO:000726; P:cell adhesion; TAS.
R GO; GO:000726; P:cell cell signaling; TAS.
R GO; GO:0006477; P:protein amino acid sulfation; TAS.
R GO; GO:0006477; P:protein amino acid sulfation; TAS.
R GO; GO:000695; P:immune response; TAS.
R GO; GO:000695; P:immune response; TAS.
R FFERP; PRO00865; Sulfortansferase.
R InterPro; IPR000865; Sulfortansferase.
R Pfem; PR00685; Sulfortansferase.
R Lectin; Selectin; Transferase.
O SEQUENCE 386 AA; 45133 MW; OC3BB4022417143A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 386 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                         61 DEGOHPDVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQ
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                                                                                   Gaps
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1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to carbohydrate (N-acetylglucosamine 6-0) sulfotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Length 386;
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96.3%; Score 1963; DB 4; Length 37:
Best Local Similarity 100.0%; Pred. No. 5.9e-176;
Matches 370; Conservative 0; Mismatches 0; Indels
                                                                           0; Indels
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Straubberg R.;
Straubberg R.;
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; EC035282; AAH352821;
GO; GO:000146; F:sulfotransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR001992; Hull basic.
InterPro; IPR001983; Sulfotransferase.
PROSITE; PS00038; Hull 1: 1.
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99.9%; Score 2035; DB 4; 99.7%; Pred. No. 1.1e-182; tive 1; Mismatches 0;
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                                         Best_Local Similaricy Autohes 385; Conservative
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SEQUENCE 3
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Best Local
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CETRAIN=C57BL/65, TISSUB=Tongue;

XX MEDLINE=21085660; PubMed=11217851;
XX MEDLINE=21085660; PubMed=11217851;
XX ARANA J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., XX Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Azawa T., Hara A., Fukunishi Y., Konno H., Kasukawa T., Yamanaka I., XX Aizawa K., Izawa M., Mishi X., Xiyosawa H., Kasukawa T., Zaito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., XX Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Xuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Stanbli F., Suuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Bronstein M.J., Bult C., Fletcher C., Fullita M., Gariboldi M., Asonstein M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamcto N., Nachioni L., Mashima J., Mazzarelli J., Mombaerts P., Nardawa Y., Sakamic N., Wilming L., Whithawa-Boris A., Yoshida K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wilming M., Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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STRANTE-STREAM FOR TISSUE=Tonsil;
MEDLINE=99264336; PubMed=10330415;
Bistrup A., Bhakta S., Lee J.-K., Belov Y.Y., Gunn M.D., Zuo F.-R.,
Huang C.-C., Kannagi R., Rosen S.D., Hemmerich S.;
"Sulforransferanses of two specificities function in the reconstitution of high endothelial cell ligands for L-selectin.";
J. Cell Biol. 145:899-910(1999).
180 RFFNIQSLYPLIKDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDSRIVMGQHEQKLKKE
                                                                                                                                       DOPYYVMOVICOSOLEIYKTIQSLPRALQERYLLVRYEDLARAPVAQTSRMYEFVGLEFL
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
N-acetylglucosamine 6-O-sulfotransferase (Carbohydrate (Chondroitin 6/keratan) sulfotransferase 4)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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EMBL, AK009113; BAB26078.1; -.
MGD, MGI.1349479; Chst4.
GO, GO.0008146; F.sulfotransferase activity; IEA.
GO, GO.001646; F.transferase activity; IEA.
InterPro; IPR000863; Sulfotransferase.
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SEQUENCE FROM N.A.
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                    MAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFVGQLFGQHPDVFYLMEPAW 60
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MEDLINES9361934; PubMed=10435581;
MEDLINES9361934; PubMed=10435581;
Hiracka N., Petryniak B., Nakayama J., Tsuboi S., Suzuki M., Yeh J.C.,
Izawa D., Tanaka T., Miyasaka M., Lowe J.B., Fukuda M.;
"A novel, high endothelial venule-specific sulfotransferase expresses
6-sulfo sialyl Lewis (X), an L-selectin ligand displayed by CD34.";
Immunity 11:79-89(1999).
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                                                                                    HVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQSSLFQWENSRALCSAP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Last annotation update)
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Best Local Simi:
Matches 281;
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                                                                                                                                                                59 QLFGQHPDVFYLMEPAWHVWMTFTSSTAWKLHMAVRDLLRSVFLCDMSVFDAYMNPGPRK 118
                                                                                                                                                                                                   QSSLFQWENSRALCSAPACDIIPQDEIIPRAHCRILCSQQPFEVVEKACRSYSHVVLKEV 179
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                                                                                                                 119 QSSLFQWEQSRALCSAPVCDFFPAHEISSPKHCKLLCGQQPFDMVEKACRSHGFVVLKEV
                                                                                                                                                                                                                                                                      299 PHLQTWVYNVTRGKGMGQHAFHTNARNALNVSQAMRWSLPYEKVSQLQDACGEAMDLLGY
                                                                                                    1 MLLPKKMKLLLFLVSQMAILALFFHMYSHNISSLSMKAQPER-MHVLVLSSWRSGSSFVG
                                                                                                                                                                                                                                                     RFFNLQSLYPLLXDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDSRIVMGQHEQKLKKE
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                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Akama T.O., Nishida K., Nakayama J., Watanabe H., Fujiwara T., Nakamura T., Dota A., Kawasaki S., Inoue Y., Maeda N., Yamamoto S., Ozaki K., Kinoshita S., Shimomura Y., Tanigami A., Fukuda M.N.; "Macular corneal dystrophy type I and type II are caused by distinct mutations in a new sulphorransferase gene.";
Nat. Genet. 26:237-241(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                  DB 11; Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
01-UIN-2003 (TrEMBLrel. 24, Last annotation update)
N-acetylglucosamine 6-0-sulforransferase GST-4beta (Corneal GST4BETA OR CHST6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hemmerich S., Lee J.-K., Bhakta S., Bistrup A., Ruddle N.R.,
Rosen S.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Chromosomal Localization and Genomic Organization for the Galactose/N-Acetylgalactosamine/N-Acetylglucosamine 6-0-Sulfotransferase Gene Family.";
                         D1E9D7796DF8574D CRC64;
                                                74.3%; Score 1513.5; DB 11
72.8%; Pred. No. 1.1e-133;
ive 49; Mismatches 53;
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GO; GO:0005794; C:Golgi apparatus; TAS
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Pfam; PF00685; Sulfotransfer; 1.
Transferase.
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BMBL, AF280006, AAG48244.1, --
EMBL, AF219990; AAG26325.1, --
EMBL, AF219991; AAG26327.1; --
                            44694 MW;
                                                               Local Similarity 72.89
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                         388 AA;
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                            SEQUENCE
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                                                                Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 GLRVVREVCRSHVRIAEAATLKP-PPFLRGRYRLVRFEDLARBPLARIRALYAFTGLSLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHLQTWVHNITRGKGMG--DHAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMNLL
                                                                                                                                                                                                                                                                                                                                                                                                             62 FGQHPDVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQS
                                                                                                                                                                                                                                                                                                                                                                                                                                            60 FNQHPDVFYLMEPAWHVWTTLSQGSAATLHMAVRDLVRSVFLCDMDVFDAYL-FWRRNLS
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                                                                                                                                                                                                                                                                                                    LLPKKMKLLLFLVSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFVGQL
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STRAIN=CSTBL/6; TISSUE=Intestine;
MEDLINE=99423499; PubMed=10491328;
Lice J.-K., Bhakta S., Rosen S.D., Hemmerich S.;
Lice J.-K., Bhakta S., Rosen S.D., Hemmerich S.;
"Cloning and Characterization of a Mammalian N-Acetylglucosamine-6-
Buffortannerserase that is Highly Restricted to Intestinal Tissue.";
Biochem. Biophys. Res. Commun. 263:543-549 (1999).
EMBL; AF176841; AADS6003.1; -.
EMBL; AF176840; AADS6002.1; -.
MGD; MGI:1931825; Chstf.
GO; GO:0008146; Fituansferase activity; IEA.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
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                                                                                                                                                                                                                                                28;
GO; GO:0001517; F:N-acetylglucosamine-6-O-sulfotransferase ac. GO; GO:0001526; P:proteoglycan sulfate transfer; TAS. InterPro; IPR000863; Sulfotransferase. Pfan; PF00685; Sulfotransferase. Transferase.
                                                                                                                                                                                               Length 395;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
N-acetylglucosamine 6-0-sulfotransferase.
CHSTS OR I-GLCNAN-6-ST.
                                                                                                                                                                                         Match 50.0%; Score 1019; DB 4; I Local Similarity 54.5%; Pred. No. 3.3e-87; les 216; Conservative 45; Mismatches 107;
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                                                                                                                                           433CA60248A48F67
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Pfam; PF00685; Sulfotransfer; 1.
Transferase.
                                                                                                                                              44098 MW;
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                                                                                                                                              395 AA;
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Pfam; PF00685; Sulfotransfer; 1.
                                                                           Conservative
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                           411 AA;
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
STRAIN=C57BL/6;
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SEQUENCE FROM N.A.
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             Transferase.
SEQUENCE 4
                                                               Best Local Sim
Matches 206;
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                                                   Query Match
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X MEDLINE=99423499; PubMed=10491328;

MEDLINE=99423499; PubMed=10491328;

A Lee J. K., Bhakta S., Rosen S.D., Hemmerich S.;

Le Cloning and Characterization of a Mammalian N-Acetylglucosamine-6-

Sulfotransferase that is Highly Restricted to Intestinal Tissue.";

E Blochem. Blophys. Res. Commun. 263:543-549(1999).

R EMBL; AF719991; AAG28023.1; --

R EMBL; AF719991; AAG28001.1; --

R EMBL; AF716838; AAD56000.1; --

R GOS GO:0016021; C:integral to membrane; TAS.

R GO; GO:0016021; C:integral to membrane; TAS.

R GO; GO:0016740; F:sulfotransferase activity; IEA.

R GO; GO:0016740; F:sulfotransferase activity; IEA.

R GO; GO:0016740; R:transferase activity; IEA.
                                                                                                                                           GOLFSQHPDVFYLMEPAWHVWDTLSQGSAPALHMAVRDLIRSVFLCDMDVFDAYL-PWRR
                        MLLPK--KWKLLLFLVSQMAILALFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFV
                                                WRLPRFSSTVMLSLLMVQTGILVF -- LVSRQVPS-SPAGLGERVHVLVLSSWRSGSSFV
                                                                          GOLFGOHPDVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPR
                                                                                                                         ROSSLFOWENSRALCSAPACDIIPQDEIIPRAHCRLLCSQOPFEVVEKACRSYSHVVLKE
 Gaps
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.. 24, Last amotcation update)
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.. forcransferase (Intestinal N-acetylglucosamine-
(N-acetylglucosamine 6-0-sulfotransferase).
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Nat. Genet. 26:237-241(2000).
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MEDLINE=20472330; PubMed=11017086;
Akama T.O., Nishida K., Nakayama J., Watanabe H., Ozaki K.,
Nakamura T., Dota A., Kawasaki S., Inoue Y., Maeda N., Yamamoto S.,
Fujiwara T., Thonar E.J., Shimomura Y., Kinoshita S., Tanigami A.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
 Indels
 Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                       411 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                              QGGZS9, Q9UBY3;
01-WAR-2001 (TEMBLEI. 16, Created)
01-WAR-2001 (TEMBLEI. 16, Last sequ
01-UUN-2003 (TEMBLEI. 24, Last sequ
Intestinal GloNAc-6-sulfotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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 Conservative
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CHSTS OR I-GLCNAC-6-ST.
Homo sapiens (Human).
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Fukuda M.N.;
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215;
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01-MAR-2001 (TERMBLrel. 16, Last sequence update)
01-OCT-2003 (TERMBLrel. 25, Last annotation update)
N-acetylglucosamine 6-0-sulfotransferase GST-5 (N-acetylglucosamine-6-0-sulfotransferase GST-5 (N-acetylglucosamine)
(N-acetylglucosamino) sulfotransferase 7).
CHST7 OR GST5 OR 2600013M07RIK.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                      LFGQHPDVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 SAFFWWATSRALCSPPACSAFPRGTISKQDVCKTLCTRQPFSLAREACRSYSHVVLKEVR.
                                                                                                                                                                    1 MLLPKKMKLLLFLVSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFVGQ
                                                                                                                                                                                                            SSLFQWENSRALCSAPACDIIPQDEIIPRAHCRLLCSQQPFEVVEKACRSYSHVVLKEVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 OPYYVMOVICOSOLEIYK--TIOSLPKALOERYLLVRYEDLARAPVAQTSRMYBFVGLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 LPHLQTWVHNITRGKGMGD--HAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMNL
                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding
                                                                                                               28;
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda
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"Identification and molecular characterization of a cDNA novel Nacetylglucosamine-6-0-sulfotransferase.";
submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                               Indels
                                                       Length
46160 MW; 97642D54BE926E06 CRC64;
                                                    Score 1008; DB 4;
Pred. No. 3.8e-86;
5; Mismatches 104;
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MEDLINE=21085660; PubMed=11217851;
                                                                                                            56;
                                                    49.5%;
52.3%;
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Thu May

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A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Gabburner M., Batalov S., Casavent T., Redota K., Matsuda H.A., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Furuo M., Aono H., Baldarelli R., Barsh G., Brake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., R., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitteker C., Wilming L., Myshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Marchional annotation of a full-length mouse cDNA collection.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 RALPSAPRADFFLTSALEVICEAWLRDLLFTRGAPAWLRRRYLRLRYEDLVWQPQAQLRR 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR280089; AAG48247.1; --
EMBL; AR011202; BAB27465.1; --
EMBL; AK011202; BAB27465.1; --
EMBL; AK011202; BAB27465.1; --
EMBL; AK01202; BAB27465.1; --
EMBL; AK01202; BAB27465.1; --
EMBL; AK01202; BAB27465.1; --
EMBL; C70350; C70350.
MGD; MGI:1891767; Chst7.
GG; G0:0008146; F:sulfotransferase activity; IEA.
GO; G0:0016740; F:transferase activity; IEA.
InterPro; IRR000863; Sulfotransferase.
Ffam; PF00685; Sulfotransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Kidney;
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AC Q99NB(
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PRT;

PRELIMINARY;

Q99NB0 Q99NB0;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233
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                                                                                                                                                                 TISSUB=Mammary gland;

Ritagawa H., Uyama T., Sugahara K.;

Submitted NAUG-2000) to the EMBL/GenBank/DDBJ databases.

BMBJ, BAB46329, BAB40372.1; -..

BMBJ, MGI:1891767; Chet7.

GO; GO:0008146; F:sulfotransferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

InterPro; IPR000883; Sulfotransferase.

Pfam; PF00685; Sulfotransferase.
                                                                  CHST7 OR MC6ST-2.
Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.6%; Score 624; DB 11; Length 4
Best Local Similarity 34.2%; Pred. No. 5.8e-50;
Matches 136; Conservative 66; Mismatches 150; Indels
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
N-acety_glucosamine-6-0-sulfotransferase (Carbohydrate (N-acety_glucosamine 6-0) sulfotransferase 7)
                                                                                                                                                                                                                                                                                                                                                                                          402CSE1ED185FDF8 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chondroitin 6-sulfotransferase-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486 AA
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SEQUENCE FROM N.A.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                         Length 486;
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                                                                   TISSUB-Brain,

A Strausberg R.;

Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.,

SmBL; AB040711; BAB13770.1; -..

R EMBL; BC045537; AAH45537.1; -..

R Gorew; HGNC:13817; CHST7.

R Go: G0:0008146; F:sulfotransferase activity; IEA.

RO; G0:0016740; F:transferase activity; IEA.

R InterPro; IPR00685; Sulfotransferase.

R Ffam; PF00685; Sulfotransferase.

Transferase.
       Uchimura K., Muramatsu T., "Identification of a cDNA "Identification and molecular characterization of a cDNA novel N-acetylglucosamine-6-0-sulfotransferase."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20347214; PubMed=10781596;
Kitagawa H., Fujita M., Ito N., Sugahara K.;
"Molecular cloning and expression of a novel chondroitin
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                   486 AA; 54266 MW; 3F1FD1430B3C8E95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                     'Match 29.8%; Score 606.5; DB 4; Local Similarity 37.0%; Pred. No. 2.6e-48; les 136; Conservative 56; Mismatches 133;
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01-OCT-2000 (TrEMBLrel, 15, Last
01-UTN-2003 (TrEMBLrel, 24, Last
Chondroitin 6-sulfotransferase-2.
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Uchimura K., Murameten H., Kadonatsu K., Fan Q., Kurosawa N.,
Mitsuoka C., Kannagi R., Habuchi O., Muramatsu T.;
"Molecular cloning and characterization of an N-acetylglucosamine-6-O-sulforransferase.",
J. Biol. Chem. 273:22577;22583(1998).

Sheli, A8011452; BAA32139.1;

EMBL, A8011451; BAA32137.1;

EMBL, A8011451; BAA32137.1;
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Mammalia, Buthazoa, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                            activity, TAS
                                                                                                                                                                                                                                                                                                              486;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last amnotation update)
N-acetylglucosamine-6-O-sulfotransferase long form.
J. Biol. Chem. 275:21075-21080(2000).

EMBL, AB037187; BAB03217.1; -
GO; GO:0016021; Cintegral to membrane; TAS.
GO; GO:0008459; F:chondroitin 6-sulfotransferase and GO; GO:0008976; P:chondroitin 6-sulfotransferase interPro; IPR000863; Sulfotransferase.

Frans. PF00685; Sulfotransferase.

Transferase.
                                                                                                                                                                                                                                                                                                  Query Match
29.7%; Score 605.5; DB 4;
Best Local Similarity 37.0%; Pred. No. 3.2e-48;
Matches 136; Conservative 56; Mismatches 133;
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GO; GO:0008146; F:sulfotransferase act
InterPro; IPR000863; Sulfotransferase.
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MEDLINE=2388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MA Klausher R.D., Collins F.S., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jeden H., Moore T., Max S.L., Rubin G.M., Heiseh F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Judin T.B., Toshiyuki S., Carninci P., Prange C.,

A romstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

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A Hilalon D.K., Muzuy D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

M. Generation and initial analysis of more than 15,000 full-length human
                                                                       9
                                                                                                  41 ERMHVLVLSSWRSGSSFVGQLFGQHPDVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRA 100
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                                                                       Gaps
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to carbohydrate (N-acetylglucosamine-6-0) sulfotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                       29;
                                           Length 530;
                                          tch 29.4%; Score 598.5; DB 11; Length al Similarity 36.8%; Pred. No. 1.6e-47; 134; Conservative 64; Mismatches 137; Indels
                A113E1B735C363EC CRC64;
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c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                57814 MW;
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             530 AA;
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Best Local Similarity
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MEDLINE=98391845; PubMed=9722682;
Uchimura K., Muramatsu H., Kaname T., Ogawa H., Yamakawa T., Fan Q.,
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biosynthesis of 6-sulfo sialyl Lewis X: Molecular cloning, chromosomal
mapping, and expression in various organs and tumor cells.";
J. Biochem. 124:670-678(1998).
J. Biochem. 124:670-678(1998).
GO: GO:0008146; P:sulfortransferase activity; IEA.
GO: GO:0008146; P:sulfortransferase activity; IEA.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                             Query Match
29.2%; Score 595.5; DB 11; Length
Best Local Similarity 36.5%; Pred. No. 3.1e-47;
Matches 133; Conservative 65; Mismatches 137; Indels
                                                       Straugherg R.; Straugherg R.; Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases. GO; GO:0008146; F:sulfotransferase activity; IEA. GO; GO:0016740; F:transferase activity; IEA. InterPro; IRR000863; Sulfotransferase.
                                                                                                                                                                                                                                                                                                  530 AA; 57828 MW; 275363BF15440730 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NAX-2000 (TrEMBLrel. 13, Created)
01-NAX-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
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29.0%; Score 591.5; DB 4; Length 4
Best Local Similarity 36.3%; Pred. No. 6.5e-47;
Matches 132; Conservative 66; Mismatches 137; Indels
                                                                                                                                                                           483 AA; 52787 MW; E27797D44931BA18 CRC64;
InterPro, IPR000863; Sulfotransferase.
Pfam; PF00665; Sulfotransfer; 1.
Transferase.
SEQUENCE 483 AA; 52787 MW; E27797D
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aay39918 Human gly	Aam93309 Human pol	4 Human	9 Human	Aay39919 Mouse gly	7 Human	7 Mouse	4	554 Human	Human d	Aay72638 Mouse gly	Murine	555	Human	Human	1560 Human	Abp56121 Human cho	S.	Aab95367 Human pro	1657	9414	10	3356	0380	Abb81558 Human cor
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ALIGNMENTS

Glycosyl sulforransferase; GST-3; detection; diagnosis; leukocyte homing; selectin binding interaction; inflammation; lymphocyte homing; human; secondary lymph organ. This sequence is the human glycosyl sulfotransferase-3 (GST-3) of the invention. The nucleic acid sequences, probes and primers derived from these, proteins and antibodies are useful in detecting homologues. The sequences, antibodies and methods are useful in the diagnosts and treatment of diseases associated with selectin binding interactions, including conditions associated with or resulting from the homing of leukcoytes to sites of inflammation and the normal homing of lymphocytes to secondary lymph organs Human and murine glycosyl sulfotransferase 3 and related polynucleotides Human glycosyl sulfotransferase-3 protein sequence. Hemmerich S; Tangemann K, AAY39918 standard, protein, 386 AA. Claim 2; Fig 1; 59pp; English. 98US-00045284. 99WO-US004316. 08-DEC-1999 (first entry) (REGC) UNIV CALIFORNIA. (SYNT) SYNTEX USA INC. Bistrup A, Rosen SD, WPI; 1999-580442/49. N-PSDB; AAZ20792. Homo sapiens. W09949018-A1. 26-FEB-1999; 20-MAR-1998; 12-NOV-1998; 30-SEP-1999 AAY39918; RESULT 1 AAY39918

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AAU11274 standard; protein; 380
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Best Local Similarity 99.7
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 Length 386;
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S, Otsuki
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100.0%; Score 2038; DB 2;
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ive 0; Mismatches 0;
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K, Kojima
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Wakamatsu A, Sugiyama
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N-PSDB; AAK94229.
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Query Match
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Matches 386; Conser
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Human, betal,3GnT; betal,3-N-acetylgluccsaminyltransferase; MECA-79; L-selectin; L-selectin sulforransferase-2; Crohn's disease; diabetes; ulcerative colitis; inflammatory skin disorder; psoriasis; Lichen planus; allergic contact dermatitis; lymphoma; chronic pneumonia; LSST-2; delayed-type hypersensitivity reaction; hyperplastic thymus; antiulcer; antinflammatory; antipsoriatic; antidiabetic; dermatological;
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been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oliqo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide enroded by a full length human cDNA of the invention. Note: The sequence data for this parent dince from part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QPYYVMQVICQSQLEIYKTIQSLPKALQERYLLVRYEDLARAPVAQTSRMYEFVGLEFLP
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                                                                                                                                                                                                                                                                                                                                                       99.9%; Score 2035; DB 4;
99.7%; Pred. No. 2.3e-205;
ive 1; Mismatches 0;
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Human transferase TRNSFS-11. 19-JUN-2000 (first entry)

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The present invention provides a method of modifying an acceptor molecule by contacting the acceptor with an isolated betal, 3-N-
by contacting the acceptor with an isolated betal, 3-N-
cety/glucosaminyltransferase (betal, 3GnT) or an active fragment, where betal, 3GnT directs expression of a MECA-79 antigen. The invention also provides a method of treating or preventing an L-selectin-mediated condition by reducing the expression or activity of a betal, 3GnT that directs expression of a MECA-79 antigen. This can be done by administering to the subject an oligosaccharide L-selectin antagonist that inhibits binding of L-selectin to a MECA-79 antigen, for example by administering antibody material that specifically binds betal, 3GnT, and/or a betal, 3GnT antisense nucleic acid molecule. L-selectin antagonist conference and olicects MECA-79 antigen expression.

Alternatively, the expression or activity of LSST-2 or its active conference in combination with reducing the expression or activity of LSST-2 or its active activity of betal, 3GnT. The method is useful for treating L-selectin mediated conditions such as Crohn's disease and ulcerative colitis.

Inflammatory disorders of the skin such as allergic contact dermatitis, psoriasis and Lichen planus, lymphomas, circuic pneumonia, dalayed-type contact environment and apprend and hyperplastic thymus. This
                                                                                                                                                                                    New enzyme, useful for modifying acceptor molecule, comprises an isolated L-selectin sulfobransferase-2 that directs expression of L-selectin ligand antigen, MECA-79 in Chinese hamster ovary cells, or intestinal GloNAc 6-sulfobransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents human LSST-2
                                                                                                                                                                                                                                                                                                                        Claim 21; Fig 4; 98pp; English.
                                                 Fukuda M, Yeh J, Hiraoka N;
(BURN-) BURNHAM INST.
                                                                                                      WPI; 2002-075226/10.
N-PSDB; AAS16947.
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DVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQSSLFQW 126
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98.5%; Score 2008; DB 5; Length 380; 100.0%; Pred. No. 1.6e-202; Live 0; Mismatches 0; Indels (
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                   Best Local Similarity 100.0
Matches 380; Conservative
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AAY79219 standard; protein; 386 AA.

RESULT 4 AAY79219 ID AAY7

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Human transferase proteins useful for preventing, diagnosing and treating cancers and developmental, gastrointestinal, genetic, immunological, neurological, reproductive and smooth muscle disorders.
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                                                                                  Transferase, TRNSFS-11; human, antitumour; cell proliferation; gastrointestinal disorder; developmental disorder; genetic disorder; neurological disorder; reproductive disorder; smooth muscle disorder; immunological disorder; inflammation; diagnosis; therapy; N-acetylglucosamine 6-0-sulfotransferase.
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                                                                                                                                                                                                                                                                 note= "potential O-phosphorylation"
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/note= "transmembrane domain"
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                                                                                                                                                                                       Location/Qualifiers
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(SYNT) SYNTEX USA INC Bistrup A, Rosen SD, WPI; 1999-580442/49 N-PSDB; AAZ20793

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23). The sequence was deduced from a cDNA clone (see AAZ94211) isolated from a gallbladder library. It shows homology to mouse Nacotylalucosamine 6-0-sulfotransferase. TRNSFS-11 is expressed in dermatologic and gastrointestinal tissues, especially those associated with inflammation and cell proliferation. The new human transferases and polymucleorides can be used in the diagnosis, prevention and treatment of cancer, developmental disorders, gastrointestinal disorders, genetic disorders, immunological disorders. neurological disorders, reproductive disorders, and semooth muscle disorders. The polypeptides can also be used to raise antibodies, and to screen for agonists and antagonists of
(see AAZ94211) isolated
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Sequence 386 AA;

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                                                                                1 MILDEKKOKLILFLVSQMAILALFFHYKSHNISSLSWKAQPERWHVLVLSSWRSGSSFVGQ
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Score 1936; DB 3; Length 386; Pred. No. 6.4e-195; 3; Mismatches 14; Indels
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    95.0%;
95.6%;
 Query Match
Best Local Similarity 95.6
Matches 369; Conservative
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Glycosyl sulfotransferase; GST-3; detection; diagnosis; leukocyte homing; selectin binding interaction; inflammation; lymphocyte homing; mouse; secondary lymph organ. glycosyl sulfotransferase-3 protein sequence. AAY39919 standard; protein; 388 AA (first entry) 08-DEC-1999 AAY39919 Mouse AAY39919

98US-00045284. WO9949018-A1. 20-MAR-1998; 12-NOV-1998; 26-FEB-1999; 30-SEP-1999

(REGC) UNIV CALIFORNIA

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                                                                                         Human and murine glycosyl sulfotransferase 3 and related polynucleotides.
                                                                                                                                               This sequence is the mouse glycosyl sulforransferase-3 (GST-3) of the invention. The nucleic acid sequences, probes and primers derived from these, proteins and antibodies are useful in detecting homologues. The sequences, antibodies and methods are useful in the diagnosis and treatment of diseases associated with selectin binding interactions, including conditions associated with or resulting from the homing of leukocytes to sites of inflammation and the normal homing of lymphocytes
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72.8%; Pred. No. 2.2e-150;
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LOVRSQQEQGNLSLDLLSSSHILGQV
                                                                                                                          Claim 2; Fig 4; 59pp; English
                                                                                                                                                                                                                                                          to secondary lymph organs
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 72.8
Matches 281; Conservative
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antiviral; antibacterial; antifungal; antithematic; antithyroid; antianaemic; antibacterial; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; Human, open reading frame, ORFX, detection, cytostatic; hepatotropic; vulnerary; antipscriatic; antiparkinsonian; nootropic; neuroprotective; antionvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressave; antinilammatory; Human ORFX ORF1711 polypeptide sequence SEQ ID NO:3422. (first entry) 08-FEB-2001

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AAB41947 standard; protein; 418

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207 FFNLQSLYPLLKDPSLNLHINHINHINHINHINHINHIN | |- || : | 365
                                                                                                                                                                                           299 LPHLQTWVHNITRGKGMGD--HAFHTNARDALNVSQAWRWSLPYBKVSRLQKACGDAMNL 356
                                                                                                                                                                                                                           New nucleic acid encoding corneal N-acetylglucosamine-6-sulfotransferase, useful for treatment, monitoring and diagnosis of macular corneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLLPK--KMKLLLFLVSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes human corneal N-acetylglucosamine-6-sulfatease(I), which is able to catalyse sulfation of keratan sulfate (KS). Also described is a method for monitoring the effect of treatments for macular corneal dystrophy (MCD), and detecting susceptibility to MCD. (I) is located to chromosome 16q22, and has ophthalmological activity. (I) can be used to treat or prevent macular corneal dystrophy types I or II. (I) makes possible treatment of MCD without requiring keratinoplasty or keratectomy. The present sequence represents mouse intestinal N-acetylglucosamine-6-sulfotransferase, which is given in comparison with (I) in the exemplification of the
                                                                                241 QPYYVMQVICQSQLEIYK--TIQSLPKALQERYLLVRYEDLARAPVAQTSRMYEFVGLBF
                                                                                                                               PHLRINEVCRSHVRIAEAATLKP-PPFLRGRYRLVRFEDLAREPLAEIRALYAFTGLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; N-acetylglucosamine-6-sulfotransferase; enzyme; GlcNAc6ST; corneal; sulfation; keratan sulfate; macular corneal dystrophy; MCD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse intestinal N-acetylglucosamine-6-sulfotransferase SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                         357 LGYRHVRSEQEQRNLLLDLL-----STWTVPE 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 24-25; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB81557 standard; protein; 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-AUG-2000; 2000US-00638211.
11-AUG-2000; 2000US-0325773P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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(AKAM/) AKAMA T O.
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Best Local 9
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ABB81557
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              cardiovascular disease, diabetes mellitus; hypothyroidism, SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDSRIVMGQHEQKLKKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-1999; 99US-0127607P.

02-APR-1999; 99US-012763FP.

05-APR-1999; 99US-0127728P.

30-MAR-2000; 200UUS-00540763.
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Best Local Similarity 61.2
Matches 241; Conservative
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                                                                                                                                                                                                                                                                                                                                                                Human; glycosyl sulfotransferase-4beta; GST-4beta; immunosuppressive; therapy; selectin binding inhibitor; gene therapy; inflammation; systemic lupus erythematosus; SLE; rhemmatoid arthritis; diabetes; polyarceritis nodosa; polymyositis; systemic sclerosis; dermatitis; glomerulonephritis; myatthenia gravis; Sjogren's syndrome; adrenalitis; Hashimoto's disease; Grave's disease; hypoparathyroidism; anaemia; myocarditis; adult respiratory distress syndrome; eczema; psoriasis; asthma; hypersensitivity; rheumatic fever; tissue rejection; chinitis; chromosome 16q23.1.
           80
200 VRFFNLOVLYPLLSDPALNLRIVHLVRDPRAVLRSREQTAKALARDNGIVLGTNGTWV-E
                                                                                                                                                                                    LPHLQTWVHNITRGKGMG--DHAFHTNARDALNVSQAWRWSLPYBKVSRLQKACGDAMNL
                                                                                                                                                                                              TPQLQTWIHNITHGSGPGARREAFKTTSRDALSVSQAWRHTLPFAKIRRVQELCGGALQL
                                          119 ROSSLFOWENSRALCSAPACDIIPQDEIIPRAHCRLLCSQOPFEVVEXACRSYSHVVLKE
                                                                                                        VRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDSRIVMGQHEQKLKK
                                                                                                                                            EDQPYYVMQVICQSQLEIYKTIQSLPKALQERYLLVRYEDLARAPVAQTSRMYEFVGLEF
                                                                                                                                                                259 ADPRILRVVNEVČRSHVRIAEALHKPPPFLQDRYRLVRYEDLARDPLTVIRELYAFTGLGL
                            GQLFGQHPDVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is human glycosyl sulfotransferase-4beta (GST-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /l sulfotransferases (GST)-4alpha, GST-4beta and GST-6 and therapeutic agent screening applications.
                                                                                                                                                                                                                                                                                                                                                     Human glycosyl sulfotransferase-4beta (GST-4beta).
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                                                                                                                                                                                                                         LGYRHVRSEQEORNLLLDLL 376
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LGYRSVHSELEORDLSLDLL 398
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13-JUN-2000; 2000US-00593828.
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N-PSDB; AAD02697, AAD02700
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cc beta). GST-4 gene is found on chromosome 16q23.1. GST is a type 2
membrane protein useful for inhibiting a binding event between a selectin
cand a selectin ligand, which comprises contacting the selectin with a non
cc sulphated selectin ligand, GST and a small molecular agent that inhibits
ct he sulphation activity of GST GST is also useful in inhibiting a
c he sulphation activity of GST GST is useful in gene therapy to treat
cc selectin mediated binding event. GST is useful in gene therapy to treat
cc disorders such as acute or chronic inflammation, systemic lugus
cerythematosus (SLB), rheumatoid arthritis, polyareritis nodosa,
cc polymyositis, dermatomyositis, systemic sclerosis, diabetes,
cc glomerulonephritis, mysathenia gravis, Sjogren's syndrome, Hashimoto's
cc glomerulonephritis, mysathenia gravis, Sjogren's syndrome, Hashimoto's
cc disease, darave's disease, adrenaltis, hypoparathyroidism, pernicious
canamis, demyelinating diseases, cirrhosis, ulcerative colitis,
cc dermatitis, myocarditis, regional enteritis, adult respiratory distress
cc syndrome, infantile eczema, psoriasis lichen planus, allergic rhintis,
cc bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection
during transplantation
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corneal; sulfation; keratan sulfate; macular corneal dystrophy; MCD;
ophthalmological; chromosome 16q22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human corneal N-acetylglucosamine-6-sulfotransferase SEQ ID NO:2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Score 1019; DB 4; Length 3
54.5%; Pred. No. 3e-98;
ive 45; Mismatches 107; Indels
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216; Conservative
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25-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                     FGQHPDVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQS 121
                                                                                                                     New nucleic acid encoding corneal N-acetylglucosamine-6-sulfotransferase, useful for treatment, monitoring and diagnosis of macular corneal
                                                                                                                                                                                                                                                                                                                                                 59
                                                                                                                                                                          The present sequence represents human corneal N-acetylglucosamine-6-sulforransferase (I), which is able to catalyse sulfation of keratan sulfate (KS). Also described is a method for monitoring the effect of treatments for macular corneal dystrophy (WCD), and detecting susceptibility to MCD. (I) is located to chromosome 16q22, and has ophthalmological activity. (I) can be used to treat or prevent macular corneal dystrophy types I or II. (I) makes possible treatment of MCD without requiring keratinoplasty or keratectomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLPKKMKLLLFLVSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFVGQL
                                                                                                                                                                                                                                                                                                                                                  LILLAQIPLILIFLVSRP------GPSSPAGGEARVHVIVLVLSWRSGSSFVGQL
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                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                       50.0%; Score 1019; DB 5; Length 395; 54.5%; Pred. No. 3e-98;
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                                                                                                                                                           Claim 13; Fig 1A-D; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; protein; 395
                                                                                                                                                                                                                                                                                                             45;
           11-AUG-2000; 2000US-00638211
11-AUG-2000; 2000US-0325773P
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                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 54.5
Matches 216; Conservative
                                                                     Fukuda MN, Akama TO;
                                                                                        WPI; 2002-507643/54.
                                        FUKUDA M N.
                                                  AKAMA T O.
                                                                                                                                                                                                                                                                      Sequence 395 AA;
                                                                                                   N-PSDB; ABN89506
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                                                                                                                                         dystrophy
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                                                  (AKAM/)
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The invention relates to human drug metabolising enzymes referred as DWE and nucleic acid molecules encoding such enzymes. Polymucleotides of the invention are useful for assessing toxicity of test compounds and in gene therapy. Sequences of the invention are useful in the diagnosis.

Consention and treatment of autoimmune/inflammatory disorders such as acquired immune deficiency syndrome (AIDS), adult respiratory distress syndrome, allergies, anaemia, atheroscilerosis, asthma, autoimmune haemolytic anaemia, conteat dermatitis, Crohn's disease, syndrome, allergies, anaemia, atheroscilerosis, asthma, autoimmune correct dermatitis, Crohn's disease, alsomentifies, docdpasture's syndrome, gout, Grave's disease, disease, theumatorio appropriate irritable bowel syndrome, multiple sclerosis, conscenthritis, osteoporosis, psoriasis, systemic lupus erythematosus, contemnatoid arthritis, osteoporosis, psoriasis, systemic lupus erythematosis, bacterial, fungal parasitic, protozoal, helminthic infections, cell proliferative disorders such as actinic keratosis, arteriosclerosis, proliferative disorders such as actinic keratosis, arteriosclerosis, confidence, any primary brain tumours, addomena, infarction associated with pregnancy, aneuryems, vascular malformations; eve disorders such as primary brain tumours, addomena, infarctions enconunctivitis, iritis, retinitis, glaucoma, pigmentose disorders such as sociated diseases, hyperchylogemenia, ipid myopathies, Menkes syndrome, hypoglycaemia, lipid myopathies, Menkes syndrome, hypoglycaemia, lipid myopathies, mannosidosis, obesity; gastrointeglinal disorders such as dysphagia,
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inflammatory disorder; acquired immune deficiency syndrome; infection; AIDS; adult respiratory distress syndrome; cell proliferative disorder; allergy; anaemia; conjunctivitis; actinic keracosis; arteriosclerosis; cancer; endocrine disorder; hypothalamus disorder; pituitary disorder; gastrointestinal disorder; metabolic disorder; developmental disorder; liver disorder; iritis; cystic fibrosis; Addison's disease; retinitis; goitre; diabetes; dysphagia; gastric carcinoma; anorexia; eye disorder;
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Sanjanwala MS;
nmar J, Griffin JA;
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e H, Tang YT, Patterson C, Das D, Sanjanw
Reddy R, Khan FA, Baughn MR, Ramkumar J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein"
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/label= Signal_peptide
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2000US-0198403P.
2000US-0200185P.
2000US-020234P.
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N-PSDB; AAD24670
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19-APR-2000;
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05-MAY-2000;
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Au-Young J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse; glycosyl sulfotransferase-4; GST-4; immunosuppressive; therapy; selectin binding inhibitor; gene therapy; inflammation; systemic lupus erythematosus; SLE; rhemmatoid arthritis, diabetes; polyarteritis nodosa; polymyositis; systemic sclerosis; dermatitis; glomerulonephritis; myasthemia gravis; Sjogren's syndrome; adrenatitis; Hashimoto's disease; Grave's disease; hypoparathyroidism; anaemia; demyelinating disease; cirrhosis; ulcerative colitis; allergic rhinitis; myocarditis; adult respiratory distress syndrome; eczema; psoriasis; asthma; hypersensitivity; rheumatic fever; tissue rejection;
                                                                                                                                                                                                             2 ILPKKMKLLLFLVSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFVGQL 61
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  gastric carcinoma, anorexia, nausea, gastroenteritis, hyperbilirubinaemia, emeals, citrhosis, diarrhosa, jaundice, Reye's syndrome, peliosis hepatitis, hepatic vein thrombosis and developmental disorders. The present sequence is human DME-5 protein
                                                                                                                                                                                                                                                  14 LLLAQIFLLLFLVSRP------GPSSPAGGEARVHVLVLSSWRSGSSFVGQL
                                                                                                                                                                           Gaps
                                                                                                                                                                         28;
                                                                                                                                   Length 395;
                                                                                                                                 Query Match
50.0%; Score 1019; DB 5; Length 39
Best Local Similarity 54.5%; Pred; No. 3e-98;
Matches 216; Conservative 45; Mismatches 107; Indels
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Best Local Similarity
                                                                                                Sequence 395 AA;
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The present sequence is mouse glycosyl sulfotransferase-4 (GST-4). GST-4 gene is found on chromosome BEI. GST is a type 2 membrane protein useful for inhibiting a binding event between a selectin and a selectin ligand, which comprises contacting the selectin with a non-sulphated selectin ligand, comprises contacting the selectin hat inhibits the sulphation activity of GST is also useful in inhibiting a selectin mediated binding event. GST is useful in gene therapy to treat disorders such as acute or chronic inflammation, systemic lupus erythematosus (SEE), rhemmatoid arthritis, polyarteritis nodosa, polymyositis, careful solerand solematomositis, systemic solerosis, diabetes, glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoro's disease, darenalitis, hypoparathyroidsm, periodicus anaemia, chempelinating diseases, cirrhosis, ulcerative colitis, dermatitis, myocarditis, regional enteritis, adult respiratory distress syndrome, infantile eczema, psoriasis lichen planus, allergic rhinitis, bronchial cransplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 VRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDSRIVMGQHEQKLKK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 LTPQLQTWIHNITHGSGPGARREAFKTTSRDALSVSQAWRHTLPFAKIRRVQELCGGALQ 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 EDQPYYVMQVICQSQLEIYK-TIQSLPKALQERYLLVRYEDLARAPVAQTSRMYEFVGLE 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 FLPHLQTWYHNITRGKGMG--DHAFHTNARDALNVSQAWRWSLFYEKVSRLQKACGDAMN 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 GOLFGOHPDVFYLMEPAWHVWMTFKOSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 NISDLFOWAVSRALCSPPVCEAFARGNISSEEVCKPLCATRPFGLAQEACSSYSHVYLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 VRFFNLQVLYPLLSDPALNLRIVHLVRDPRAVLRSREQTAKALARDNGIVLGTNGTWV-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 ADPRLRVVNEVCRSHVRIAEAALHKPPPFLÖDRYRLVRYEDLARDPLTVIRELYAFTGLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MRLPRFSSTVMLSLLMVQTGILVF---LVSRQVPS-SPAGLGERVHVLVLSSWRSGSSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 ROSSLFQWENSRALCSAPACDIIPQDEIIPRAHCRLLCSQQPFEVVEKACRSYSHVVLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MLLPK--KMKLLLFLVSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Gaps
                                                                                                                                New glycosyl sulfotransferases (GST)-4alpha, GST-4beta and GST-6 for diagnostic and therapeutic agent screening applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine intestinal-GlcNAc 6-sulfotransferase (I-GlcNAc6ST) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
49.9%; Score 1017.5; DB 4; Length 395;
Best Local Similarity 56.4%; Pred. No. 4.3e-98;
Matches 215; Conservative 43; Mismatches 112; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 LLGYRHVRSEQEQRNLLLDLL 376
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                      Hemmerich S;
                                                                                                                                                                                                         Claim 3; Fig 2; 128pp; English.
                                                                   WPI; 2001-138471/14.
                      Lee JK,
                                                                                          N-PSDB; AAD02696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 395 AA;
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                      Rosen SD,
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Mouse; betal,3GnT; betal,3-N-acetylglucosaminyltransferase; MECA-79; L-selectin; L-selectin sulforransferase-2; Crohn's disease; diabetes; ulcerative colitis; inflammatory skin disorder; psortasis; Lichen planus; allergic contact dermatitis; lymphoma; chronic pneumonia; LSST-2; delayed-type hypersensitivity; reaction; hyperplastic thymus; antiulcer; antiinflammatory; antipsoriatic; antidiabetic; dermatological; antiallergic; intestinal-GloNAc 6-sulfotransferase; I-GloNAc6ST.
                                                                                                                                    10-MAY-2001; 2001WO-US015452.
                                                                                                                                                       11-MAY-2000; 2000US-00569320
                                                                                                                                                                         (BURN-) BURNHAM INST
                                                                                                                                                                                                             WPI; 2002-075226/10.
                                                                                                                                                                                                                      N-PSDB; AAS16948
                                                                                                  WO200185177-A1
                                                                                Mus musculus
                                                                                                                    15-NOV-2001.
                                                                                                                                                                                            Fukuda M,
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Yeh J, Hiraoka

The present invention provides a method of modifying an acceptor molecule by contacting the acceptor with an isolated betal, 3-Nacetylglucosaminyltransferase (betal, 3GTD) or an active fragment, where betal, 3GTD directs expression of a NECA-79 antigen. The invention also provides a method of treating or preventing an L-selectin-mediated condition by reducing the expression or activity of a betal, 3GTT that directs expression of a NECA-79 antigen. This can be done by administering to the subject an oligosaccharide L-selectin antagonist that inhibits binding of L-selectin to a MECA-79 antigen, for example by administering to the subject an oligosaccharide L-selectin antagonist and/or a betal, 3GTT antisense nucleic acid molecule L-selectin califoransferase-2 (LSST-2) also directs MECA-79 antigen expression.

Alternatively, the expression or activity of LSST-2 or its active conformed in combination with reducing the expression or activity of betal, 3GTT. The method is useful for treating L-selectin mediated conditions such as Crohn's disease and ulcerative colitis, psoriasis and Lichen planus, lymphomas, chronic pneumonia, delayed type hypersensitivity reactions, diabetes and hyperplastic thymus. This sequence represents mouse I-GlorAc6ST New enzyme, useful for modifying acceptor molecule, comprises an isolated L-selectin sulfctransferase-2 that directs expression of L-selectin ligand antigen, MECA-79 in Chinese hamster ovary cells, or intestinal GloNAC 6-sulfctransferase. 28 1 MLLPK--KMKLLLFLVSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFV 49.9%; Score 1017.5; DB 5; Length 395; 56.4%; Pred. No. 4.3e-98; tive 43; Mismatches 112; Indels 11; Gaps Claim 28; Fig 10; 98pp; English. Matches 215; Conservative Similarity Sequence 395 AA; Query Match Best Local (

118 26 119 ROSSLFOWENSRALCSAPACDIIPQDEIIPRAHCRLLCSQOPFEVVEKACRSYSHVVLKE GOLFGOHPDVFYLMEPAWHVWMTFKOSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPR 29 g 셤 ò ò à

Ser

/label= Asn,

179 VRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDSRIVMGQHBQKLKK 238

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295 IIPOLGIWIHNITHGSGPGARREAFKITSRDALSVSGAWRHILPFAKIRRVQELGGGALQ 354 239 EDQPYYVMQVICQSQLEIXK-TIQSLPKALQERYLLVRYEDLARAPVAQTSRMYBFVGLE 235 ADPRILRVVNEVČRSHVRIAEAALHKPPPPLQDRYRLVRYEDLARDPLTVIRELYAFTGLG 298 FLPHLOTWVHNITRGKGMG--DHAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMN Human, N-acetylglucosamine-6-sulfotransferase, enzyme; GlcNAc6ST; corneal; sulfation; keratan sulfate; macular corneal dystrophy; MCD; Consensus N-acetylglucosamine-6-sulfotransferase SEQ ID NO:3. Gly Ser Met Ą. His, Thr, LLGYRHVRSEQEORNLLLDLL 376 Asp, Met, Ser, Thr, Pro, His, Ser, Glu label= Ala, Thr, Glu Lys ABB81555 standard; protein; 395 label= Arg, label= Ala, abel= Gly, label= Ala, label= Ser, label= Ala, label= Val, 'label= Ala, abel= Ala, label= Thr, label= Gly, label= Ser, label= Ala, label= Leu, label= Thr, label= His, Misc-difference 394 Misc-difference 392 Misc-difference 238 Misc-difference 39 ophthalmological. Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Homo sapiens. Mus musculus. Synthetic. 05-SEP-2002 356 ABB81555, RESULT 13 ABB81555 셤 8 셤 8 ઠ 셤

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 FNLQVLYPLLSDPALNLRIVHLVRDPRAVLRSREQTAKALARDNGIVLGTNGTWV-EADP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 PYYYMQVICQSQLEIYK--TIQSLPKALQERYLLVRYEDLARAPVAQTSRMYEFVGLEFL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHLQTWVHNITRGKGMG--DHAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMNLL 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 SLFQWENSRALCSAPACDIIPQDEIIPRAHCRLLCSQQPFEVVEKACRSYSHVVLKEVRF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FNLOSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDSRIVMGQHEQKLKKEDQ 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 FGQHPDVFYLMEPAWHVWMTFKQSTAWMLHWAVRDLIRAVFLCDMSVFDAYMEPGPRRQS 121
                                                                                                                                                                                       New nucleic acid encoding corneal N-acetylglucosamine-6-sulfotransferase, useful for treatment, monitoring and diagnosis of macular corneal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 LLLAQIXLLLFLVSRP------GPSSPAGGEXRVHVLVLSSWRSGSSFVGQL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LLPKKMKLLLFLVSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFVGQL 61
                                                                                                                                                                                                                                                    The present invention describes human corneal N-acetylglucosamine-6-sulforransferase (I), which is able to catalyse sulfation of keratan sulfate (KS). Also described is a method for monitoring the effect of treatments for macular corneal dystrophy (MCD), and detecting susceptibility to MCD. (I) is located to chromosome log2, and has ophthalmological activity. (I) can be used to treat or prevent macular corneal dystrophy types I or II. (I) makes possible treatment of MCD without requiring keratinoplasty or keratectomy. The present sequence represents a consensus N-acetylglucosamine-6-sulfotransferase which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                  49.7%; Score 1013.5; DB 5; Length 395; 55.9%; Pred. No. 1.1e-97; ative 45; Mismatches 101; Indels 21;
                                                                                                                                                                                                                                    Example 5; Fig 2A-B; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GYRHVRSEQEQRNLLLDLL 376
                                                                             11-AUG-2000; 2000US-00638211.
                                                       09-AUG-2001; 2001US-00927602
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                              Fukuda MN, Akama TO;
                                                                                                                                                                  WPI; 2002-507643/54
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                             (FUKU/) FUKUDA M N.
(AKAM/) AKAMA T O.
                                                                                                                                                                                                                                                                                                                                                                                Sequence 395 AA;
              US2002061562-A1
                                                                                                                                                                                                                                                                                                                                                                                                                          212;
                                   23-MAY-2002
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The present sequence is human glycosyl sulfotransferase-4alpha (GST-4 alpha). GST-4 gene is found on chromosome 16q23.1. GST is a type 2 alpha). GST-4 gene is found on chromosome 16q23.1. GST is a type 2 and a selectin useful for inhibiting a binding event between a selectin and a selectin ligand, which comprises contacting the selectin with a non sulphated selectin ligand, sor GST is also useful in inhibiting a selectin mediated binding event. GST is also useful in inhibiting a selectin mediated binding event. GST is useful in gene therapy to treat disorders such as acute or chronic inflammation, systemic lupus contents such as acute or chronic inflammation, systemic lupus cypthomatics, dermatomyositis, polyarestifs nodosa, polymyositis, dermatomyositis, systemic selectis, diabetes, glomerulonephritis, myasthenia gravis, Sjogren's syndrome, Hashimoto's disease, dermaltins, myocarditis, phypotacthyroidism, permicious anaemia, demyelinating diseases, cirrhosis, ulcerative collitis, commantitis, myocarditis, recema, psoriaeis lichen planus, allergic rhinitis, bronchial asthma, hypersensitivity, rheumatic fever and tissue rejection curing transplantation. Note: The present sequence is also shown in correction (bring transplantation. Note: The present sequence is also shown in correction control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MLLPKKMKLLLFLVSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFVGQ
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Best Local Similarity 52.3%; Pred. No. 4.2e-97;
Matches 206; Conservative 56; Mismatches 104; Indels 28;
                                                                                                                                                                       Human glycosyl sulfotransferase-4alpha (GST-4alpha).
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N-PSDB; AAD02697, AAD02698, AAD02699.
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13-JUN-2000; 2000US-00593828.
                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome 16q23.1
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                                                                                           02-MAY-2001
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AAY72639 standard; protein; 390 AA

RESULT 14 AAY72639 ID AAY7 XX Length 390;

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                                                119 SAFFNWATSRALCSPPACSAFPRGTISKQDVCKTLCTRQPFSLARBACRSYSHVVLKEVR 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes human corneal N-acetylglucosamine-6-sulfotransferase (I), which is able to catalyse sulfation of keratan sulfate (KS). Also described is a method for monitoring the effect of treatments for macular corneal dystrophy (MCD), and detecting susceptibility to MCD. (I) is located to chromosome 16422, and has ophthalmological activity. (I) can be used to treat or prevent macular corneal dystrophy types I or II. (I) makes possible treatment of MCD without requiring keratinoplasty or keratectomy. The present sequence represents human intestinal N-acetylglucosamine-6-sulfotransferase, which is given in comparison with (I) in the exemplification of the
                                                                                                                                                                                     241 OPYYVMQVICQSQLEIYK--TIQSLPKALQERYLLVRYEDLARAPVAQTSRMYEFVGLEF
SSLFQWENSRALCSAPACDIIPQDEIIPRAHCRLLCSQQPFEVVEKACRSYSHVVLKEVR
                                                                                                                                     FFNLOSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDSRIVMGQHEQKLKKED
                                                                                                                                                                                                                                                                                                                                                                                                                   299 LPHLQTWVHNITRGKGMGD--HAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, N-acetylglucosamine-6-sulfotransferase, enzyme; \operatorname{GlcNAc6ST}_i corneal; \operatorname{sulfation}_i keratan \operatorname{sulfate}_i macular \operatorname{corneal}_i \operatorname{dystrophy}_i \operatorname{MCD}_i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human intestinal N-acetylglucosamine-6-sulfotransferase SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 LGYRPVYSADQQRDLTLDLVLPRGPDHFSWASPD 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGYRHVRSEQEQRNLLLDLL-----STWTVPE 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Fig 2A-B; 69pp; English.
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(AKAM/) AKAMA T O.
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                                                                                        LEGOHPDVEYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQ 120
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                                                                                                                                                                                                                                 241 OPYYVMOVICOSOLEIYK--TIOSLPKALOERYLLVRYEDLARAPVAOTSRMYEFVGLEF
                                                                14 ILLAQITCLLLFIISRP------GPSSPAGGEDRVHVLVLSSWRSGSSFLGQ
                                            1 MLLPKKMKLLLFLVSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFVGQ
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                       Indels
49.5%; Score 1008; DB 5; 1
52.3%; Pred. No. 4.2e-97;
ive 56; Mismatches 104;
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Sequence 2, Application US/09816825;
Patent No. US20010051370A1;
GRDEAL INCRAMITON,
APPLICANT: Bistrup, Annette
APPLICANT: Rosen, Steven D.
APPLICANT: Hemmerich, Stefan
TITLE OF INVENTION: GLYCOSYL SULFOTRANSFBRASE-3
FILE REFERENCE: 6510-107COM
CURRENT FAILING DATE: 2001-03-22
PRIOR PLILING DATE: 2001-03-22
PRIOR PLILING DATE: 1998-03-20
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                         6, 2004, 10:51:28 ; Search time 48 Seconds (without alignments) 2232.099 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 255, App Sequence 97, Appl Sequence 128, App Sequence 6, Appli Sequence 5, Appli Sequence 3, Appli Sequence 4, Appli Sequence 8, Appli Sequence 2, Appli Sequence 2, Appli Sequence 11, Appl Sequence 5, Appli Sequence 2, Appli Sequence 2, Appl: Description Sequence 3 US-10-007-262-1 4 US-10-427-631-11 US-09-927-602-5 US-10-258-080-5 US-10-258-080-5 US-09-927-602-3 US-09-927-602-4 US-09-927-602-4 US-09-927-602-8 US-10-212-933-4 US-09-833-790-255 US-10-211-462-97 US-10-211-462-97 US-10-211-462-97 US-09-816-825-2 Query Match Length DB Score Result No.

Sequence 7, Appli	Sequence 123, App	Sequence 126, App	Sequence 9, Appli	Sequence 10, Appl	Sequence 11, Appl	Sequence 21, Appl	Sequence 21, Appl	Sequence 6, Appli	Sequence 6, Appli	O.	σ,	w	.,	7	Sequence 16, Appl	ñ	ä	స	H	ĭ	Sequence 2, Appli	Sequence 2, Appli	Sequence	20, A <u>r</u>	e 7	Æ;	53.5	Sequence 1903, Ap	m	
	2 US-10-087-192-1					.4 US-10-126-279-21	4 US-10-286-606-21	.0 US-09-811-469-6	.4 US-10-370-659-6	.2 US-10-425-114-39283	.2 US-10-225-066A-854	.5 US-10-225-067-56	.5 US-10-374-780A-330	.2 US-10-424-599-149380	.6 US-10-380-727-16	.2 US-10-042-865-38	.5 US-10-262-445-132	.5 US-10-259-194A-380	.4 US-10-411-976-11	.5 US-10-369-493-1075	.4 US-10-126-279-2	.4 US-10-286-606-2	.5 US-10-369-493-23144	US-09-854-122-20	.2 US-10-282-122A-76479	US-10-223-0	US-10-425-1	94	J US-09-849-626-1903	
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ALIGNMENTS

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100.0%; Score 2038; DB 9; Length 386;
Best Local Similarity 100.0%; Pred. No. 4.6e-202;
Matches 386; Conservative 0; Mismatches 0; Indels 0 , ORGANISM: Homo sapiens US-09-816-825-2 SEQ ID NO 2 LENGTH: 386 121 121 TYPE: PRT a d ö ò ò

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ORGANISM: Homo sapiens
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                                                                                                                                           HLQTWVHNITRGKGMGDHAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMNLLGYR 360
                                                                                                     241 QPYYVMQVICQSQLBIYKTIQSLPKALQERYLLVRYEDLARAPVAQTSRMYBFVGLEFLP 300
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                                                                        QPYYVMQVICQSQLEIYKTIQSLPKALQERYLLVRYEDLARAPVAQTSRMYEFVGLEFLP
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FPNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTKGDLMIDSRIVMGQHEQKLKKED
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APPLICANT: Rosen, Steven D.
APPLICANT: Assembly Kirsten
APPLICANT: Tangemann, Kirsten
APPLICANT: Tangemann, Kirsten
APPLICANT: Tangemann, Kirsten
APPLICANT: Hemmerich, Stefan
TITLE OF INVENTION: GLYCOSYL SULFOTRANSFERASE-3
FILE REPREBRUE: 6510-107CTP
CURRENT APPLICANTION NUMBER: 2001-11-08
FRIOR APPLICANTION NUMBER: EARLIER APPLICATION NUMBER: 09/190,911
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRSESEQ for Windows Version 3.0
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100.0%; Score 2038; Pest Local Similarity 100.0%; Pred. No. 4.6
Matches 386; Conservative 0; Mismatches
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Publication No. US20020164748A1
GENERAL INFORMATION:
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; ORGANISM: H. sapiens
US-10-007-262-1
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; OTHER INFORMATION: Incyte ID No. US20030175923A1 2617407CD1
.US-10-427-631-11
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                                                                                                                                      APPLICANT: COKEDY, Natial C.; GUEGLER, Karl J.;
APPLICANT: COKEDY, Natial C.; GUEGLER, Karl J.;
APPLICANT: BAUGHN, Marial R.; LaL, Preeti G.;
APPLICANT: AZIMZAL, Yalda
APPLICANT: AZIMZAL, Yalda
TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
FILE REFERENCE: PF-0592-1 DIV
CURRENT APPLICATION NUMBER: US/10/427,631
CURRENT APPLICATION NUMBER: US/09/786,240
PRIOR APPLICATION NUMBER: US 09/786,240
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 60/172,220
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-05-10
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
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PRIOR FILING DATE: 1999-05-11
PRIOR FILING DATE: 1999-05-11
PRIOR PILING DATE: 1998-05-11
PRIOR PILING DATE: 1998-05-11
                                                                                                                APPLICANT: INCYTE CORPORATION; TANG, Y. TOM; APPLICANT: CORLEY, Neil C.; GUEGLER, Karl J.;
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Sequence 11, Application US/10427631 Publication No. US20030175923A1 GENERAL INFORMATION:
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Patent No. US20020061562A1
GENERAL INFORMATION:
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Best Local Similarity 95.6
Matches 369; Conservative
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Local Similarity 54.5
hes 216; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               59 GQLFGQHPDVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPR
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                                                                                                                                                                                                                                                             Length 418;
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TITLE OF INVENTION: Methods of Treating Macular Corneal
TITLE OF INVENTION: Methods of Treating Macular Corneal
TITLE OF INVENTION: Dystrophy
FILE REFERENCE: P-LJ 4852
CURRENT PELICATION NUMBER: US/09/927,602
CURRENT FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: US 09/638,211
PRIOR FILING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO SEQ ID NOS: 38
LENGTH: 418
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2e-97;
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US-09-927-602-5
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DB 9; Length 395;

50.0%; Score 1019;

Query Match

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                                                                            2 LLPKKMKILLFIVSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFVGQL
                             28;
Pred. No. 1.6e-96;
5; Mismatches 107; "Indels
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APPLICANT: BANKUMAR, Jayalaxmi
APPLICANT: GRIFFIN, Jennifer A.
APPLICANT: GRIFFIN, Jennifer A.
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES
FILE REFERENCE: PI-0070 USN
CURRENT APPLICATION NUMBER: US/10/258,080
CURRENT APPLICATION NUMBER: US 60/203,509
PRIOR APPLICATION NUMBER: US 60/203,509
PRIOR FILING DATE: 2000-05-11
PRIOR FILING DATE: 2000-05-16
PRIOR FILING DATE: 2000-05-17
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: US 60/200,185
PRIOR APPLICATION NUMBER: US 60/200,185
PRIOR APPLICATION NUMBER: US 60/200,185
PRIOR APPLICATION NUMBER: US 60/198,403
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APPLICATION NUMBER: PCT/US01/11869
FILING DATE: 2001-04-12
APPLICATION NUMBER: US 60/197,590
FILING DATE: 2000-04-13
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SANJANWALA, Madhusudan M
GANDHI, Ameena R.
REDDY, ROOPA M.
KHAN, Farrah A.
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LAL, Preeti G.
TRIBOULEY, Catherine M
YAO, Monique G.
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APPLICANT: POLICKY, Jennifer L.
APPLICANT: HAFALIA, April J.A.
APPLICANT: BURFORD, Neil
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     54.5%;
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Mismatches
                                                                14 LLLAQTXLLLFLVSRP------
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   45;
   212; Conservative
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TYPE: PRT
CRGANISM: Homo Sapien
US-09-927-602-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNLQVLYPLLSDPALNLRIVHLVRDPRAVLRSREQTAKALARDNGIVLGTWGTWV-EADP 237
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                                                                                                                  NAME/KEY: misc feature
O'S-10-258-080-5
US-10-258-080-5
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APPLICANT: Akama, Tomoya O.
TITLE OF INVENTION: Methods of Treating Macular Corneal
TITLE OF INVENTION: Dystrophy
FILE REPERBLOE: P-LJ 4852
CURRENT APPLICATION NUMBER: US/09/927,602
CURRENT APPLICATION NUMBER: US 09/638,211
PRIOR APPLICATION NUMBER: US 09/638,211
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 395
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1013.5; DB 9;
Pred. No. 5.9e-96;
                                                                                                                                                                                  Similarity 54.5%; Score 1019; DB 12;
Similarity 54.5%; Pred. No. 1.6e-96;
6; Conservative 45; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 GYRHVRSEQEQRNLLLDLL-----STWTVPEQIH 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GYRPVYSEDEQRNLALDLVLPRGLNGFTWASSTASH 392
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; OTHER INFORMATION: Xaa = any amino acid
US-09-927-602-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: synthetic construct
NAME/KEY: VARIANT
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Patent No. US20020061562A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 20
SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 395
                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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Matches 216;
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US-09-927-602-3
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                                                                                                                                                        62 FGQHPDVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRAVFLCDMSVFDAYMEPGPRRQS
                                                                                                                                                                                                        60 FSQHPDVFYLMEPAWHVWTTLSQGSAATLHMAVRDLXRSVFLCDMDVFDAYL-PWRRNLS
                                                                                                                                                                                                                                                                                                           119 DLFQWAVSRALCSPPACSAFPRGXISSEXVCKPLCARQPFXLAREACRSYSHVVLKEVRF
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                                                  2 LLPKKMKLLLFLVSQMAILALFFHMYSHNISSLSMKAQPERMHVLVLSSWRSGSSFVGQL
                                                                                                ---GPSSPAGGEXRVHVLVLSSWRSGSSFVGQL
                                                                                                                                                                                                                                                              122 SLFQWENSRALCSAPACDIIPQDEIIPRAHCRLLCSQQPFEVVEKACRSYSHVVLKEVRF
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21;
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Sequence No. US20020061562A1

GENERAL INFORMATION:

APPLICANT: Akama, Tomoya O.

TITLE OF INVENTION: Methods of Treating Macular Corneal

TITLE OF INVENTION: Methods of Treating Macular Corneal

TITLE OF INVENTION: Methods of Jetrophy

FILE REFERENCE: P-LJ 4852

CURRENT FILINON UNMBER: US/09/927,602

CURRENT FILINO ADPRE: 2001-08-09

PRIOR FUING DATE: 2001-08-09

PRIOR FUING DATE: 2000-08-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FaatSEQ for Windows Version 4.0

FENDENT 300
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Indels
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49.5%; Score 1008; DB 9; I
Best Local Similarity 52.3%; Pred. No. 2.1e-95;
Matches 206; Conservative 56; Mismatches 104;
  101;
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415 SGSSSKPFVVSARNATQAANAWRTALTFQQIKQVEEFCYQPMAVLGYERVNSPEEVKDLS 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 BRMHVLVLSSWRSGSSFVGQLFGQHPDVFYLMEPAWHVWMTFKQSTAWNLHMAVRDLIRA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 KCPPQRLARPEEECRKYRTVVIKGVRVFDVAVLAPLLKDPALDLKVIHLVRDPRAVASSR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 QLEIYKTIQSLPKALQERYLLVRYEDLARAPVAQTSRMYEFVGLEFLPHLQTWVHNITRG 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 KGMGDHAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMNLLGYRHVRSEQEQRNLL 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 -CSQQPFEVVEKACRSYSHVVLKEVRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSR
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             FILE REFERENCE: TOYAM1.001AUS
CURRENT APPLICATION NUMBER: US/10/212,933
CURRENT FILING DATE: 2002-08-05
PRIOR APPLICATION NUMBER: US/09/263,023
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2: SEQ ID NO 2: 10
TITLE OF INVENTION: DNA ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10212933 Publication No. US20030008366A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      ) ORGANISM: Mus musculus
US-10-212-933-2
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                                                                                                                                                                                                                                                                                    TYPE: PRT
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                       PHLRLIRBVCRSHVRIAEAATLKP-PPFLRGRYRLVRFEDLAREPLAEIRALYAFTGLTL 296
                                                                                                      297 TPQLEAWIHNITHGSGIGKPIEAFHTSSRNARNVSQAWRHALPFTKILRVQEVCAGALQL 356
241 QPYYVMQVICQSQLEIYK--TIQSLPKALQERYLLVRYEDLARAPVAQTSRMYEFVGLEF 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152 CRLLCSQQPFEVVEKACRSYSHVVLKEVRFFNLQSLYPLLKDPSLNLHTVHLVRDPRAVF 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 RSRERTKGDLMIDS------krigslpkalgery 126
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                                                                                LPHLQTWVHNITRGKGMGD - - HAFHTNARDALNVSQAWRWSLPYBKVSRLQKACGDAMNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 SSLSMKAQPERMHVLVLSSWRSGSSFVGQLFGQHPDVFYLMEPAWHVWMTFKQSTAWMLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 MAVRDLIRAVFLCDMSVFDAYMEPGPRRQSSLFQWENSRALCSAPACDIIPQDEIIPRAH
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                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09927602
| Patent No. US2002061562A1
| GENERAL INFORMATION:
| APPLICANT: FUXUAG, Michiko N. |
| APPLICANT: Akama, Tomoya O. |
| TITLE OF INVENTION: Methods of Treating Macular Corneal
| TITLE OF INVENTION: Dystrophy |
| TITLE OF INVENTION: Dystrophy |
| TITLE OF INVENTION: Dystrophy |
| FILE REPRENCE: P-LJ 4852 |
| CURRENT APPLICATION NUMBER: US/09/927,602 |
| CURRENT FILING DATE: 2001-08-09 |
| PRIOR FILING DATE: 2000-08-11 |
| NUMBER OF SEQ ID NOS: 38 |
| SEQ ID NOS: 38 |
| LENGTH: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF N-ACETYLGLUCOSAMINE-6-0-
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LGYRPVYSADQQRDLTLDLVLPRGPDHFSWASPD 390
                                                                                                                                                          357 LGYRHVRSEQEQRNLLLDLL-----STWTVPE 383
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APPLICANT: Muramatsu, Hideki
APPLICANT: Radomatsu, Kenji
APPLICANT: Kannagi, Renji
APPLICANT: Habuchi, Osami
APPLICANT: Muramatsu, Takashi
TITLE OF INVENTION: SULFOTRANSFERASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10212933
Publication No. US20030008366A1
GENERAL INFORMATION:
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CORGANISM: Homo Sapien
US-09-927-602-8
                                                                                                                                                                                                                                                            RESULT 9
US-09-927-602-8
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Sequence 97, Application US/10211462; Publication No. US20040033495A1; GENERAL INFORMATION:
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US-10-211-462-97
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Fatent No. US2002066288A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wohamath, Raddon
APPLICANT: Wohamath, Raddon
APPLICANT: Mohamath, Raddon
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: ADD DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING APRE. 2001-04-11
NUMBER OF SEQ ID NOS: 440
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                                                                                                                                  Query Match 28.8%; Score 587.5; DB 14; Best Local Similarity 36.0%; Pred. No. 1e-51; Matches 131; Conservative 67; Mismatches 137;
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28.8%; Score 587.5; DB 9;
Best Local Similarity 36.0%; Pred. No. 1.2e-51;
Matches 131; Conservative 67; Mismatches 137;
                                 3.0
PRIOR FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 4
LENGTH: 484
                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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US-09-833-790-255
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LENGTH: 531
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GENERAL INFOURATION:

APPLICANT: Mirray, Richard

APPLICANT: Wateson, Susan R.

APPLICANT: Wateson, Susan R.

APPLICANT: Wateson, Susan R.

APPLICANT: Wateson, Susan R.

APPLICANT: Bos Biotechnology, Inc.

ITLE OF INVENTION: Methods of Exceeding for Angiogenesis Modulators

ITLE OF INVENTION: Wateson S. Soreening for Angiogenesis Modulators

ITLE OF INVENTION: Wateser: US/10/211,462

CURRENT APPLICATION NUMBER: US/00/22-13

FRIOR APPLICATION NUMBER: US 09/794,356

PRIOR FILING DATE: 2001-02-14

PRIOR FILING DATE: 2001-02-24

PRIOR FILING DATE: 2001-02-24

PRIOR PILING DATE: 2001-02-30

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 97

LEMATH 411
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101 VFLCDMSVFDAYMEPGPRRQS----SLFQWENSRALCSAPACDIIPQDEIIPRAHCRLL- 155
                                      224 LYRCDLSVFQLYSPAGSGGRNLTTLGIFGAATNKVVCSSPLCPAY-RKEVVGLVDDRVCK 282
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                                                                                                                            -CSOOPFEVVEKACRSYSHVVLKEVRFFNLOSLYPLLKDPSLNLHIVHLVRDPRAVFRSR
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Query Match
Best Local Similarity 41.1%
Matches 113; Conservative
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, ORGANISM: Homo Sapien
US-09-927-602-6
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US-09-927-602-6
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US-10-021-660-128

Sequence 128, Application US/10021660

Publication No. US20030152926A1

GENERAL INFORMATION:
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
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                                    273 LVRYEDLARAPVAQTSRMYEFVGLEFLPHLQTWVHNITRG-KGMGDHAFHTNARDALNVS 331
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                                                                                                                                                                      246 TFRDTYRLWRLWYGTGR------KPYNLDVTQLTTVCEDFSNSVSTGLMRPPWLKGKYM 298
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SQOPFEVVEKACRSYSHVVLKEVRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSRER 216
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                                                                                                                    217 TKGDLMIDSRIVMGQHEQKLKKEDQPYYV----MQVICQSQLEIYKTIQSLPKALQERYL
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34.3%; Pred. No. 7.8e-48;
ive 64; Mismatches 160;
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Best Local Similarity 34.34
Matches 139; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 169;
358 EKWRFRLSYDIVAPAQNACQOVLAQLGYKIAASEBELKNPSVSLV 402
                                                                                                                                                           Sequence 6, Application US/09927602

| Redent No. US20020061562A1
| Patent No. US20020061562A1
| GENERAL INPERMATION:
| APPLICANT FURUAL MICHIKO N.
| APPLICANT: Akama, Tomoya O.
| TITLE OF INVENTION: Methods of Treating Macular Corneal
| TITLE OF INVENTION: Methods of Treating Macular Corneal
| TITLE OF INVENTION: MARIES US/09/927,602
| CURRENT APPLICATION WUMBER: US/09/927,602
| CURRENT FILING DATE: 2001-08-09
| PRIOR FILING DATE: 2000-08-11
| PRIOR FILING DATE: 2000-08-11
| NUMBER OF SEQ ID NOS: 38
| SOFTWARE: PastSEQ for Windows Version 4.0
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41.1%; Pred. No. 2.5e-45;
live 15; Mismatches 34;
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Sequence

Sequence Seq

US-08-471-066B-5 US-08-484-956-5 US-08-599-491-5 US-08-759-491-5 US-08-823-516-5 US-08-823-516-5 US-08-759-038-5 US-08-759-038-5 US-08-759-038-5 US-08-759-038-5 US-08-368-5 US-09-368-5 US-09-758-2828-5
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APPLICANT: Bistrup, Annette
APPLICANT: Rosen, Steven D.
APPLICANT: Rosen, Steven D.
APPLICANT: Hemmerich, Stefan
TITLE OF INVENTION: GLYCOSYL SULFOTRANSFERASE-3
FILE REFERRNCE: 6510-1071031
CURRENT APPLICATION NUMBER: US/09/045,284A
CURRENT APPLICATION NUMBER: 1998-03-20
NUMBER OF SEQ ID NOS: 9
SEQ ID NO: 5EQ ID NOS: 9
SEQ ID NO: 5EQ ID NOS: 9
LENGTHARE: FastSEQ for Windows Version 4.0
SEQ ID NO SEG ID NOS: 9
LENGTHARE: ABCOMMENT OF SEG ID NOS: 10 NOT NUMBER OF SEQ ID NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 10 NOS: 
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CRGANISM: Homo sapiens

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Copyright (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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38;	Mismatches	NIS	NIS	H H	-H	AHC	HG-	VFR	VFR	OERYL	RYL	VSO	VSQ-	9
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US-09-180-911-1
US-09-263-023-2
US-09-263-023-4
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US-09-471-867-4
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Query Match 1

Result No.

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TITLE OF INVENTION: HUMAN TRANSFERASE PROTEINS
FILE REFERENCE: PF-0592 PCT
CURRENT APPLICATION NUMBER: US/09/786,240
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 1998-09-10; 1998-11-04; 1998-11-04; 1999-15-11
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PERL PROGRAM
SEQ ID NO 11
LENGTH: 386
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APPLICANT: Uchimura, Kenji
APPLICANT: Muramatsu, Hideki
APPLICANT: Radomatsu, Kenji
APPLICANT: Kandagi, Rejij
APPLICANT: Kannagi, Rejij
APPLICANT: Kannagi, Rejij
APPLICANT: Kannagi, Rejij
APPLICANT: Muramatsu, Takashi
APPLICANT: Muramatsu, Takashi
APPLICANT: Nuramatsu, Takashi
ITILE OF INVENTION: POLYEPPTIDE OF N-ACETYLGLUCOSAMINE-6-0-SULFOTRANSFERASE AND
ITILE OF INVENTION: DNA ENCODING THE SAME
FILLE REFERENCE: TOYAM1.0101AUS
CURRENT APPLICATION NUMBER: US/09/263,023
CURRENT PILING DATE: 1999-03-05
BARLIER PILING DATE: 1998-03-05
BARLIER APPLICATION NUMBER: UP 10-177844
BARLIER APPLICATION NUMBER: UP 10-177844
SARLIER PILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6558935 2617407CD1
US-09-786-240-11
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 95.6%; Pred. No. 3.4e-201;
Matches 369; Conservative 3; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 HVRSEQEQRNLLLDLLSTWTVPEQIH 386
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Patent No. 6037159
GENERAL INFORMATION:
                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Bietrup, Sreven D.
APPLICANT: Annemmann, Kirsten
APPLICANT: Hangemann, Kirsten
APPLICANT: Hemmerich, Stefan
TITLE OF INVENTION: GLYCOSYL SULFOTRANSFERASE-3
FILE REFRENCE: 6510-107CIP
CURRENT APPLICATION NUMBER: 09/045,284
EARLIER APPLICATION NUMBER: 09/045,284
SALIER FILING DATE: 1998-03-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 386
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100.0%; Score 2038; DB 4
Best Local Similarity 100.0%; Pred. No. 3e-212;
Matches 386; Conservative 0; Mismatches 0
  HVRSEQEQRNLLLDLLSTWTVPEQIH 386
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Patent No. 6558935
GENERAL INFORMATION:
APPLICANT: INCYIE PHARMACEUTICALS, INC
APPLICANT: GONLEY, Neil C.
APPLICANT: GONLEY, Neil C.
APPLICANT: GONLEY, Neil J.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: IAL, Preeti
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: AZIMZAI, Yalda
                                                                                                                       Sequence 1, Application US/09190911
Patent No. 6365365
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: H. sapiens
US-09-190-911-1
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US-09-786-240-11
                                                                         RESULT 2
US-09-190-911-1
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APPLICANT: Uchimura, Kenji
APPLICANT: Muramatsu, Hideki
APPLICANT: Muramatsu, Kenji
APPLICANT: Kadomatsu, Kenji
APPLICANT: Kadomatsu, Kenji
APPLICANT: Kannagi, Relji
APPLICANT: Kannagi, Relji
APPLICANT: Habuchi, Osami
APPLICANT: Muramatsu, Takashi
TITLE OF INVENTION: DNA ENCODING THE SAME
FILE REFERNES: TOTAMA: Old AUG.
CURRENT APPLICATION NUMBER: US/09/263,023
CURRENT PILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: JP 10-177844
EARLIER FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
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                                                                                        VFLCDMSVFDAYMEPGPRRQS----SLFQWENSRALCSAPACDIIPQDEIIPRAHCRLL-
                                                                                                                                             176 LYRCDLSVPQLYSPAGSGGRNLTTLGIPGAATNKVVCSSPLCPAY-RKEVVGLVDDRVCK
                                                                                                                                                                                                      -CSQQPFEVVEKACRSYSHVVLKEVRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSR
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Patent No. 6037159
GENERAL INFORMATION:
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Matches 131, Conservative
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APPLICANT: Waramateu, Hideki
APPLICANT: Maramateu, Hideki
APPLICANT: Kadomateu, Kenji
APPLICANT: Kanagi, Reiji
APPLICANT: Kanagi, Reiji
APPLICANT: Rancahi, Osami
APPLICANT: Maramateu, Takashi
TITLE OF INVENTION: POLYPEPTIDE OF N-ACETYLGLUCOSAMINE-6-0-SULFOTRANSFERASE AND
TITLE OF INVENTION: DAG BECODING THE SAME
FILE REPERBNCE: TOYAM41, 001AUS
CURRENT FILING DATE: 1999-03-05
EARLIER PILING DATE: 1999-03-05
EARLIER FILING DATE: 1999-03-05
EARLIER FILING DATE: 1999-03-05
EARLIER FILING DATE: 1998-03-05
EARLIER APPLICATION NUMBER: UChosami
                                                                                                                                                                                                                                                        41 ERMHVLVLSSWRSGSSFVGQLFGQHPDVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRA 100
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                                                                                                                                                                                                                                                                                                                                                                                                      41 ERMHVLVLSSWRSGSSFVGQLFGQHPDVFYLMEPAWHVWMTFKQSTAWMLHMAVRDLIRA 100
                                                                                                                                                                                                                                                                                                                                                               VFLCDMSVFDAYMEPGPRRQS----SLFQWENSRALCSAPACDIIPQDEIIPRAHCRLL- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -CSQQPFEVVEKACRSYSHVVLKEVRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 KCPPQRLARFEEECRKYRTVVIKGVRVFDVAVLAPLLKDPALDLKVIHLVRDPRAVASSR 294
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                                                                                                                                                Length 483;
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                                                                                                                                                DB 3;
                                                                                                                                                                                                   64; Mismatches 137;
                                                                                                                                                                           .4e-56;
                                                                                                                                       Query Match
29.4%; Score 598.5;
Best Local Similarity 36.8%; Pred. No. 4.4
Matches 134; Conservative 64; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09471867
Patent No. 6455289
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Best Local Similarity 36.8%
Matches 134; Conservative
                                ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-263-023-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mus musculus
US-09-471-867-2
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     LENGTH: 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 TKGDLMIDSRIVMGQHEQXLKKEDQPYYV----MQVICQSQLBIYKTIQSLPKALQBRYL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 TFRDTYRLWRLWYGTGR-----KPYNLDVTQLTTVČEDFSNSVSTGLMRPPWLKGKYM 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 LVRYEDLARAPVAQTSRMYEFVGLEFLPHLQTWVHNITRG-KGMGDHAFHTNARDALNVS 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 LSSWRSGSSFVGQLFGQHPDVFYLMBPAWHVWWT----FKQSTA----WMLHMAVRDLIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 SOQPFEVVEKACRSYSHVVLKEVRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSRER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 QAWRWSLPYEKVSRLQKACGDAMNLLGYRHVRSEQEQRNLLLDLL 376
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Williams, Kevin J
APPLICANT: Tabas, Ira
APPLICANT: Tabas, Ira
TITLE OF INVENTION: A Human Gene Encoding Human Chondroitin
TITLE OF INVENTION: 6-Sulfotransferase
FILE REFERENCE: JEFF-0231
CURRENT APPLICATION NUMBER: US/09/015,188C
CURRENT FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
LENGTH: 411
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APPLICANT: HABUCHI, OSAMI
LITE OF INVENTION: DNA CODING FOR SULFOTRANSFERASE
NUMBER OF SEQUENCES: 9
CORRESSONDENCE ADDRESS:
STREET:
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.9%; Score 549; DB 4; 34.3%; Pred. No. 7.9e-51; iive 64; Mismatches 160;
                                                                                                                                                                                                                                                           Sequence 2, Application US/09015188C Patent No. 6399358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 34.3%
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-015-188-2
                                   373 LDLL 376
                                                                                                   476 KTLL 479
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APPLICANT: Uchimura, Kenji
APPLICANT: Uchimura, Kenji
APPLICANT: Kadomatsu, Hideki
APPLICANT: Kadomatsu, Kenji
APPLICANT: Kannagi, Reiji
APPLICANT: Kannagi, Reiji
APPLICANT: Kannagi, Reiji
APPLICANT: Mabuchi, Osami
APPLICANT: Mabuchi, Halekini
APPLICANT: Mabuchi, Haleki
                                                                                                                                          356 MAKTLOTALQPPDWLQGHYLVVRYEDLVGDPVKTLRRVYDFVGLLVSPEWEQFALNMTSG 415
                                                                                                                                                                                                                                                                          416 SGSSSKPFVVSARNATQAANAWRTALIFPQQIKQVEEFCYQPMAVLGYERVNSPEEVKDLS 475
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253 QLEIYKTIQSLPKALQERYLLVRYEDLARAPVAQTSRMYEFVGLEFLPHLQTWVHNITRG 312
                                                                                                                                                                                                                               313 KGMGDHAFHTNARDALNVSQAWRWSLPYEKVSRLQKACGDAMNLLGYRHVRSEQEQRNLL 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
28.8%; Score 587.5; DB 4; Length 4
Best Local Similarity 36.0%; Pred. No. 6.8e-55;
Matches 131; Conservative 67; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09471867
Patent No. 6455289
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-867-4
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                                                                                                                                                                                                                                                                                                                                                                                                                           476 KTLL 479
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Sequence 6, Application US/09811469
Patent No. 6551809
GENERAL INFORMATION:
APPLICANT: YAN, Chumhua et al.
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: WUCLBIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 IRAVFLCDMSVFDAYMEPGPRRQSSLFQWE--NSRALCSAPACDIIPQDEIIPRAHCR-L 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 MVAFAGKYKTWKKWLDDEGQDGLREEEVQR-----LRGNCESIRLSAELGLRQ-PAWL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268 QERYLLVRYEDLARAPVAQTSRMYEFVGLEFLPHLQTWVHNITRGKGMGDHAFHTNARDA 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 IKQLFLCDLYVLEHPITPLPEDHLTQFMFRRGSSRSLCEDPVCTPFVK-KVPEKYHCKNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 LCSQQPFEVVEKACRSYSHVVLKEVRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQFEKWRFSMPFKLAQVVQAPCGPAMRLFGYXLARDAAALTNRSVSLL 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 23.7%; Score 482; DB 2; Length 47
Best Local Similarity 32.4%; Pred. No. 1.8e-43;
Matches 113; Conservative 71; Mismatches 141; Indels
           SSEE: KNOBBE, MARTENS, OLSON & BEAR, LLP
F: 620 NEWPORT CENTER DRIVE, SIXTEENTH FLOOR
NEWPORT BEACH
CALIFORNIA
                                                                                                                         ZIP: 32660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTENTING
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,514
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DÂTE:
ATTORNEY AGENT INFORMATION:
NAME: DANIEL E ALTWAN
REGISTRATION NUMBER: 34,115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKST NUMBER: TC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714 760 0404
TELEPAX: 714 760 9502
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-899-514-2
CORRESPONDENCE ADDRESS:
ADDRESSEE: KNOBBE, M
STREET: 620 NEWPORT
CITY: NEWPORT BEACH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                      STATE: CA
COUNTRY:
ZIP: 926
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US-09-811-469-6
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Patent No. 5910581
GENERAL INFORMATION:
APPLICANT: HABUCHI, OSAMI
APPLICANT: FUKUTA, MASAXAZU
TITLE OF INVENTION: POLYPEPTIDE OF GLYCOSAMINOGLYCAN
TITLE OF INVENTION: SULFOTRANSFERASE ORIGINATING FROM HUMAN AND DNA CODING
TITLE OF INVENTION: FOR THE POLYPEPTIDE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 MAV -- RDLIRAVFLCDMSVFDAYMEPGPRRQ -- SSLFQWENSRALCSAPACDIIPQ - DEI 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 DPRAVFRSRERTKGDLMIDSRIVMGQHEQKLK-----KEDQPYYVMQVICQS-QLE 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPRAVLVSR------WV---AFSGKYESWKKWAAEGEAPLQEDE-VQRLRGNCESIRLS 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 IYKTIQSLPKALQERYLLVRYEDLARAPVAQTSRMYEFVGLEFLPHLQTWVHNITRGKGM 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 GDHAFHTWARDALNVSQAWRWSLPYEKVSRLQKACGDAMNLLGYRHVRSEQEQRNLLLDL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 LSMKAQPERMHVLVLSSWRSGSSFVGQLFGQHPDVFYLMEPAWHV--WMTFKQSTAWMLH 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 IPRAHÇR-LLÇSQQPFEVVEKAÇRSYSHVVLKEVRFFNLQSLYPLLKDPSLNLHIVHLVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.6%; Score 500.5; DB 2; 33.2%; Pred. No. 1.7e-45; iive 75; Mismatches 133;
                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,878
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 33.2%
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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NG-09-150-141-11

Sequence II. Application US/09150141B

Sequence III. Application US/09150141B

Patent No. 6071732

GENERAL INFORMATION:

TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES, NUCLEIC ACIDS ENCODING

TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES, AND METHODS OF USE THEREOF

TITLE OF INVENTION UNMER: US/09/150,141B

CURRENT APPLICATION NUMBER: US/09/150,141B

CURRENT PAPLICATION NUMBER: US/09/150,141B

CURRENT PALING DATE: 1998-09-09

NUMBER OF SEQ ID NOS: 45

SEQ ID NOS: 45

SEG ID NO: 11

LENGTH: 359
                                                                                                                                                                                                                                              Sequence 11, Application US/09150133B
Sequence 11, Application US/09150133B
Sequence 11, Application US/09150133B
Setent No. 6060295
GENERAL INFORMATION:
APPLICANT: The Board of Regents of the University of Oklahoma
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERAES, AND METHODS OF USE THEREOF
FILE REFERENCE: 5820.504
CURRENT APPLICATION NUMBER: US/09/150,133B
CURRENT APPLICATION NUMBER: US/09/150,133B
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 5.1 (saved in ASCII format)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 RSGSSFVGQLFGQHPDV----FYLMEPAWHVWMTFKQSTAWMLHWAVRDLIRAVFLCDMS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPDAYMEPGPRRQSSLFQWENSRALCSAPACDIIPQ-DEIIPRAHCRLLCSQQPFEVVEK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 ACRSYSHVVLKEVRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSRERTK----GDLM 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----YTALWLPTIR-----RLYP------NAKFILMIRDARAVVHSMIERKVPVAGYNT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 LARAPVAQTSRMYEFVGLEFLPHLQTWVHNITRGKGMGDHAFH-TNARDALNVSQAWRWS 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 LIQKPAEEILKITNFLDLPFSQQMLRHQDLIGDEVDLNDQBFSASQVKNSINTKALTSWF 311
                                      234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 IDSRIVMGQHEQKLKKKEDQPYYVMQVICQSQ----LEIYKTIQSLPKALQERYLLVRYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --YER
             180 RFFNLQSLYPLLKDPSLNLHIVH----LVRDPRAVFRSRERTKGDLMID-SRIVMGQHEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98;
                                                                                                                                       711 NLPABVQE--ELETLCASMKABIGAKCRLVHLSLVKTEKSMLKMLEPRF 757
                                                                                                    -OLEIYKTIQSLPKALQERY 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.5%; Score 92; DB 3; Le
19.5%; Pred. No. 0.22;
Live 48; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338 LPY-EKVSRLOKACGDAMNLLGY 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Caenorhabditis elegans
                                                                                                         235 KLKKEDQPYYVMQVICQS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 19.54
Matches 63; Conservative
                                                                                                                                                                                                                                     -09-150-133-11
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Patent No. 6383753
GENERAL INFORMATION:
APPLICANT: Thiele, Dennis
APPLICANT: Liu, Phillip
TITLE OF INVENTION: No. 6383753el Yeast and Mammalian Regulators of Cell Proliferat
FILE REPERENCE: UM-04266
CURRENT APPLICATION NUMBER: US/09/540,824
CURRENT FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.0
SEQ ID NO 27
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                                                                                                                                                                                                                                                                Gaps 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323
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                                                                                                                                                                                                                                                                                                         156 CSQQPFEVVEKACRSYSHVVLKEVRFFNLQSLYPLLKDPSLNLHIVHLVRDPRAVFRSRE 215
                                                                                                                                                                                                                                                                                                                                                356 CLKKAIEITECMEAQNMNVLLLEE---NASDLCCLISS-----LVQLMMDPHC----RT 402
                                                                                                                                                                                                                                                                                                                                                                                            216 RIKGDLMIDSRIVMG------OHEOKLKKEDQPYYVMQVICQSQLEIYKTIQSLPKAL 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 ARDALNVSQAWRWSLPYE-KVSRLQKACGDAMNLL------GYRHVRSEQEQRNLLL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482 IROHWKGRODKOKSSPVSFGLISAIRLVSGLFPVADSW--HPVV---VPALFLATEALCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --YMEPGPRROSSLFQWENSRALCSAP----ACDIIPQD
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                                                                                                                                                                                                                                                                                                                                                                                                                        268 Q--ERYLLVRYEDLARAPVAQTSRMYEFVGLEFLPHLQTWVHNITRGK--GMGDHAFHTN
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                                                                                                                                                                                                                                                                65;
                                                                                                                                                                                                                     DB 4; Length 668;
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                                                                                                                                                                                                                       Query Match
4.9%; Score 100.5; DB 4;
Best Local Similarity 22.7%; Pred. No. 0.067;
Matches 57; Conservative 35; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --SGOOS--
CURRENT APPLICATION NUMBER: US/09/811,469
CURRENT FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 EFTETÝLTVLSDSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-540-824-27
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553 PLTQSKSSPKR 563
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Best Local Similarity
Matches 74; Conserv
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                                                                                                                                                         ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .09-540-824-27
                                                                                                                                                                                US-09-811-469-6
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Parent No. 6204016

GENERAL INFORMATION:
APPLICANT: THE BOARD of Regents of the University of Oklahoma
ITLE OF INVENTION: TYROSYLPROETIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
FILE REFERENCE: 5820.546
CURRENT APPLICATION NUMBER: US/03/374,493
EARLIER APPLICATION NUMBER: 09/150,133
EARLIER FILING DATE: 1998-09-09
EARLIER FILING DATE: 1998-01-29
EARLIER FILING DATE: 1998-01-29
EARLIER FILING DATE: 1998-01-29
EARLIER FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Wordperfect 8.0 (saved in ASCII format)
SEQ ID NO 11.
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4.5%; Score 92; DB 3; Length 359;
Best Local Similarity 19.5%; Pred. No. 0.22;
Matches 63; Conservative 48; Mismatches 114; Indels
                                                           Query Match
4.5%; Score 92; DB 3; Length 359;
Best Local Similarity 19.5%; Pred. No. 0.22;
Matches 63; Conservative 48; Mismatches 114; Indels
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217 SDEISMFVQWNQELRK------MTFQCNNAPGQCIKVY------
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; ORGANISM: Caenorhabditis elegans
US-09-374-493-11
ORGANISM: Caenorhabditis elegans
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